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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:24:53 ; Search time 36.95 seconds
(without alignments)
21.885 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 863609 seqs, 134777022 residues

Total number of hits satisfying chosen parameters: 863609

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 Summaries

Database :
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27: /cgn2_6/ptodata/2/paa/US060_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	40	100.0	9	1 PCT-US96-17882-38	Sequence 38, Appl
2	40	100.0	9	17 US-09-258-947-38	Sequence 38, Appl
3	40	100.0	10	1 PCT-US96-17882-1	Sequence 1, Appl
4	40	100.0	10	17 US-09-258-947-1	Sequence 1, Appl
5	35	87.5	601	17 US-09-252-691-6267	Sequence 6267, Ap
6	34	85.0	10	1 PCT-US96-17882-4	Sequence 4, Appl

7	34	85.0	10	17	US-09-258-947-4	Sequence 4, Appl
8	34	85.0	113	16	US-09-173-300-54	Sequence 54, Appl
9	34	85.0	144	18	US-09-417-507-38814	Sequence 38814, A
10	33	82.5	42	16	US-09-138-721-3	Sequence 3, Appl
11	33	82.5	42	16	US-09-138-721-4	Sequence 4, Appl
12	33	82.5	60	21	US-60-147-499-4281	Sequence 4281, Ap
13	33	82.5	60	21	US-60-197-873-15322	Sequence 15322, A
14	33	82.5	130	21	US-60-160-202-4217	Sequence 4217, Ap
15	33	82.5	130	21	US-60-160-203-5931	Sequence 5931, Ap
16	33	82.5	130	21	US-60-169-840-8929	Sequence 8929, Ap
17	33	82.5	130	21	US-60-169-842-4971	Sequence 4971, Ap
18	33	82.5	228	17	US-09-248-796-20444	Sequence 20444, A
19	33	82.5	228	17	US-60-096-409-20444	Sequence 20444, A
20	33	82.5	253	1	PCT-US00-13737-10	Sequence 10, Appl
21	33	82.5	357	16	US-09-107-532-5132	Sequence 5132, Ap
22	33	82.5	365	21	US-60-208-020-114	Sequence 114, App
23	33	82.5	365	21	US-60-209-043-149	Sequence 149, App
24	33	82.5	370	12	US-08-732-368-2	Sequence 2, Appl
25	33	82.5	384	18	US-09-429-555-2	Sequence 2, Appl
26	33	82.5	423	18	US-09-328-603-2	Sequence 2, Appl
27	33	82.5	442	21	US-60-208-020-141	Sequence 141, App
28	33	82.5	442	21	US-60-209-043-181	Sequence 181, App
29	33	82.5	455	17	US-09-206-647-4	Sequence 4, Appl
30	33	82.5	469	8	US-08-448-489-12	Sequence 12, Appl
31	33	82.5	469	13	US-08-814-394A-23	Sequence 23, Appl
32	33	82.5	469	15	US-09-068-851-10	Sequence 10, Appl
33	33	82.5	469	18	US-09-391-104-23	Sequence 23, Appl
34	33	82.5	469	19	US-09-521-220-16	Sequence 16, Appl
35	33	82.5	469	21	US-60-230-435-1022	Sequence 1104, Ap
36	33	82.5	476	18	US-09-328-603-4	Sequence 4, Appl
37	33	82.5	847	21	US-60-212-655-540	Sequence 540, App
38	33	82.5	847	21	US-60-229-515-1088	Sequence 1088, Ap
39	33	82.5	853	18	US-09-354-129-10	Sequence 10, Appl
40	33	82.5	853	19	US-09-504-357-10	Sequence 10, Appl
41	33	82.5	872	21	US-60-207-317-386	Sequence 386, App
42	33	82.5	1816	21	US-60-167-217-2657	Sequence 2657, Ap
43	33	82.5	1816	21	US-60-173-464-2156	Sequence 2156, Ap
44	33	82.5	1816	21	US-60-191-637-2622	Sequence 2622, Ap
45	33	82.5	1816	21	US-60-191-637-2622	Sequence 2622, Ap

ALIGNMENTS

RESULT 1
PCT-US96-17882-38
; Sequence 38, Application PC/TUS9617882
; GENERAL INFORMATION:
; APPLICANT: THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
; TITLE OF INVENTION: MINOTOPES AND ANTI-MIMOTOPES OF HUMAN
; TITLE OF INVENTION: PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17882
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/556,597
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.

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; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-17882-38

Query Match 100.0%; Score 40; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 3 WRYREY 8

RESULT 2
US-09-258-947-38
; Sequence 38, Application US/09258947
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF HUMAN PLATELET
; FILE REFERENCE: 011.00117
; CURRENT APPLICATION NUMBER: US/09/258,947
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/406,330
; EARLIER FILING DATE: 1995-03-17
; EARLIER APPLICATION NUMBER: 08/556,597
; EARLIER FILING DATE: 1995-11-13
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Mimotopes and
; OTHER INFORMATION: Anti-mimotopes of Human Platelet Glycoprotein
; OTHER INFORMATION: Ib/IX
US-09-258-947-38

Query Match 100.0%; Score 40; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 3 WRYREY 8

RESULT 3
PCT-US96-17882-1
; Sequence 1, Application PC/TUS9617882
; GENERAL INFORMATION:
; APPLICANT: THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF HUMAN
; TITLE OF INVENTION: PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
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; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17882
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/556,597
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-17882-1

Query Match 100.0%; Score 40; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 4 WRYREY 9

RESULT 4
US-09-258-947-1
; Sequence 1, Application US/09258947
; GENERAL INFORMATION:
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF HUMAN PLATELET
; TITLE OF INVENTION: GLYCOPROTEIN IB/IX
; FILE REFERENCE: 011.00117
; CURRENT APPLICATION NUMBER: US/09/258,947
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/406,330
; EARLIER FILING DATE: 1995-03-17
; EARLIER APPLICATION NUMBER: 08/556,597
; EARLIER FILING DATE: 1995-11-13
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Mimotopes and
; OTHER INFORMATION: Anti-mimotopes of Human Platelet Glycoprotein
; OTHER INFORMATION: Ib/IX
US-09-258-947-1

Query Match 100.0%; Score 40; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 wryrey 6
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Db 4 WRYREY 9

RESULT 5
US-09-252-691-6267
; Sequence 6267, Application US/09252691B
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
; FILE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/09/252,691B
; CURRENT FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 11324
; SEQ ID NO 6267
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-09-252-691-6267

Query Match 87.5%; Score 35; DB 17; Length 601;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
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Db 250 WRYRHY 255

RESULT 6
PCT-US96-17882-4
; Sequence 4, Application PC/TUS9617882
; GENERAL INFORMATION:
; APPLICANT: THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF HUMAN
; TITLE OF INVENTION: PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17882
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/556,597
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

PCT-US96-17882-4

Query Match 85.0%; Score 34; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
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Db 4 WRYSEY 9

RESULT 7
US-09-258-947-4
; Sequence 4, Application US/09258947
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF HUMAN PLATELET
; TITLE OF INVENTION: GLYCOPROTEIN Ib/IX
; FILE REFERENCE: 011.00117
; CURRENT APPLICATION NUMBER: US/09/258,947
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/406,330
; EARLIER FILING DATE: 1995-03-17
; EARLIER APPLICATION NUMBER: 08/556,597
; EARLIER FILING DATE: 1995-11-13
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Mimotopes and
; OTHER INFORMATION: Anti-mimotopes of Human Platelet Glycoprotein
; OTHER INFORMATION: Ib/IX
US-09-258-947-4

Query Match 85.0%; Score 34; DB 17; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
 |||||
Db 4 WRYSEY 9

RESULT 8
US-09-173-300-54
; Sequence 54, Application US/09173300
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
; FILE REFERENCE: BB-1126
; CURRENT APPLICATION NUMBER: US/09/173,300
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 60/063,423
; EARLIER FILING DATE: 1997 October 28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 54
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Lactococcus lactis
US-09-173-300-54

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Best Local Similarity 66.7%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 29 WRYKDY 34

RESULT 9
US-09-417-507-38814
; Sequence 38814, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 38814
; LENGTH: 144
; TYPE: PRT
; ORGANISM: A.fumigatus
US-09-417-507-38814

Query Match      85.0%; Score 34; DB 18; Length 144;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 4 WKRYQY 9

RESULT 10
US-09-138-721-3
; Sequence 3, Application US/09138721
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 North Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,721
; FILING DATE: 24-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/942,330
; FILING DATE: 5-SEPT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,721
; FILING DATE: 24-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/942,330
; FILING DATE: 5-SEPT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-138-721-3

Query Match      82.5%; Score 33; DB 16; Length 42;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 17 WRYDEY 22

RESULT 11
US-09-138-721-4
; Sequence 4, Application US/09138721
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 North Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,721
; FILING DATE: 24-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/942,330
; FILING DATE: 5-SEPT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-138-721-4

Query Match      82.5%; Score 33; DB 16; Length 42;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 17 WRYDEY 22

RESULT 12
US-60-147-499-4281
; Sequence 4281, Application US/60147499
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
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; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/60/147,499
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4281
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-147-499-4281

Query Match 82.5%; Score 33; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryre 5
|
|
|
|
Db 31 WRYRE 35

RESULT 13
US-60-197-873-15322
; Sequence 15322, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81. US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 15322
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-197-873-15322

Query Match 82.5%; Score 33; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryre 5
|
|
|
|
Db 31 WRYRE 35

RESULT 14
US-60-160-202-4217
; Sequence 4217, Application US/60160202
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEEN
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; FILE REFERENCE: CL000114
; CURRENT APPLICATION NUMBER: US/60/160,202
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4392
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4217
; LENGTH: 130
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-202-4217

Query Match 82.5%; Score 33; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 wryre 5
|
|
|
|
Db 99 WRYRE 103

RESULT 15
US-60-160-203-5931
; Sequence 5931, Application US/60160203
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000116
; CURRENT APPLICATION NUMBER: US/60/160,203
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 6374
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5931
; LENGTH: 130
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-203-5931

Query Match 82.5%; Score 33; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryre 5
|
|
|
|
Db 99 WRYRE 103

Search completed: November 8, 2000, 07:26:36
Job time: 103 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:27:03 ; Search time 35.8 seconds
(without alignments)
22.588 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 863609 seqs, 134777022 residues

Total number of hits satisfying chosen parameters: 44447

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

RefSeq_Patents_AA.*

- 1: /cgn2_6/ptodata/2/paa/US06_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US07_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 8: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 9: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 10: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 11: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 12: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 13: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 14: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 15: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
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- 19: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
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- 23: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
- 24: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
- 25: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
- 26: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*
- 27: /cgn2_6/ptodata/2/paa/US09_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

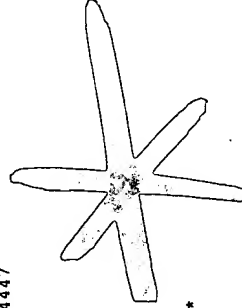
SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	65.0	6	17	US-09-258-947-174
2	23	57.5	5	13	US-08-877-605-21
3	23	57.5	5	14	US-08-981-122-12
4	23	57.5	5	14	US-08-981-122-12
5	23	57.5	5	15	US-09-096-749A-80
6	23	57.5	5	15	US-09-096-749A-86

7	23	57.5	5	15	US-09-096-749A-88	Sequence 88, Appl
8	23	57.5	5	15	US-09-096-749A-92	Sequence 92, Appl
9	23	57.5	6	1	PCT-US99-04656-15	Sequence 15, Appl
10	23	57.5	6	9	US-08-482-230-124	Sequence 124, App
11	23	57.5	6	10	US-08-563-128-124	Sequence 124, App
12	23	57.5	6	10	US-08-564-690-124	Sequence 124, App
13	23	57.5	6	10	US-08-564-693-124	Sequence 124, App
14	23	57.5	6	10	US-08-564-765-124	Sequence 124, App
15	23	57.5	6	15	US-09-007-288B-54	Sequence 54, Appl
16	23	57.5	6	15	US-09-007-288B-54	Sequence 54, Appl
17	23	57.5	6	17	US-09-227-357-428	Sequence 428, App
18	21	52.5	6	1	PCT-US99-27631-16	Sequence 16, Appl
19	21	52.5	6	9	US-08-460-112A-29	Sequence 29, Appl
20	21	52.5	6	16	US-09-196-934-16	Sequence 16, Appl
21	20	50.0	4	4	US-08-082-440-10	Sequence 10, Appl
22	20	50.0	5	13	US-08-877-605-23	Sequence 23, Appl
23	20	50.0	6	1	PCT-US99-27631-5	Sequence 5, Appl
24	20	50.0	6	9	US-08-476-438-17	Sequence 17, Appl
25	20	50.0	6	9	US-08-488-659-17	Sequence 17, Appl
26	20	50.0	6	12	US-08-721-019-17	Sequence 17, Appl
27	20	50.0	6	12	US-08-721-019-162	Sequence 162, App
28	20	50.0	6	16	US-09-185-908-40	Sequence 40, Appl
29	20	50.0	6	16	US-09-185-908-161	Sequence 161, App
30	20	50.0	6	16	US-09-196-934-5	Sequence 5, Appl
31	20	50.0	6	17	US-09-282-029-40	Sequence 40, Appl
32	20	50.0	6	17	US-09-282-029-161	Sequence 161, App
33	20	50.0	6	18	US-09-379-968-3	Sequence 3, Appl
34	20	50.0	6	18	US-09-379-968-6	Sequence 6, Appl
35	20	50.0	6	18	US-09-434-355-40	Sequence 40, Appl
36	20	50.0	6	18	US-09-434-355-161	Sequence 161, App
37	20	50.0	6	18	US-09-434-355-483	Sequence 483, App
38	20	50.0	6	18	US-09-434-355-517	Sequence 517, App
39	19	47.5	3	1	PCT-US97-23182-27	Sequence 27, Appl
40	19	47.5	3	1	PCT-US98-12122-27	Sequence 27, Appl
41	19	47.5	3	20	US-09-657-276-1181	Sequence 1181, Ap
42	19	47.5	5	12	US-08-799-054-75	Sequence 75, Appl
43	19	47.5	5	15	US-09-020-880-75	Sequence 75, Appl
44	19	47.5	5	15	US-09-020-880-75	Sequence 75, Appl
45	19	47.5	5	15	US-09-096-749A-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-258-947-174
; Sequence 174, Application US/09258947
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF HUMAN PLATELET
; TITLE OF INVENTION: GLYCOPROTEIN IB/IX
; FILE REFERENCE: 011.00117
; CURRENT APPLICATION NUMBER: US/09/258,947
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/406,330
; EARLIER FILING DATE: 1995-03-17
; EARLIER APPLICATION NUMBER: 08/556,597
; EARLIER FILING DATE: 1995-11-13
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Mimotopes and
; OTHER INFORMATION: Anti-mimotopes of Human Platelet Glycoprotein
; OTHER INFORMATION: Ib/IX
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(4)
; OTHER INFORMATION: variable amino acid



US-09-258-947-174

Query Match 65.0%; Score 26; DB 17; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.5e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 wryrey 6
|||
Db 1 WRXXEY 6

RESULT 2
US-08-877-605-21
; Sequence 21, Application US/08877605
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide x Library
US-08-877-605-21

Query Match 57.5%; Score 23; DB 13; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryr 4
| | |
Db 2 WHYR 5

RESULT 3
US-08-981-122-12
; Sequence 12, Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; EARLIER FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP96/01734
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetptide
; OTHER INFORMATION: synthesizing system (RAMPS)
US-08-981-122-12

Query Match 57.5%; Score 23; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wry 3
|||
Db 1 WRY 3

RESULT 4
US-08-981-122-12
; Sequence 12, Application US/08981122B
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; CURRENT FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetptide
; OTHER INFORMATION: synthesizing system (RAMPS)
US-08-981-122-12

Query Match 57.5%; Score 23; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wry 3
|||
Db 1 WRY 3

RESULT 5
US-09-096-749A-80
; Sequence 80, Application US/09096749A
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-096-749A-80

Query Match 57.5%; Score 23; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wtyr 4
Db 2 WRWR 5

RESULT 6
US-09-096-749A-86
Sequence 86, Application US/09096749A
GENERAL INFORMATION:
APPLICANT: Koleda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749A
FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-096-749A-86

Query Match 57.5%; Score 23; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 wtyr 4
Db 2 WRWR 5

RESULT 7
US-09-096-749A-88
Sequence 88, Application US/09096749A
GENERAL INFORMATION:
APPLICANT: Koleda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749A
FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-096-749A-88

Query Match 57.5%; Score 23; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wtyr 4
Db 2 WRWR 5

RESULT 8
US-09-096-749A-92
Sequence 92, Application US/09096749A
GENERAL INFORMATION:
APPLICANT: Koleda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis

STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096.749A
FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-096-749A-92

Query Match 57.5%; Score 23; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
Db 2 WRWR 5

RESULT 9
PCT-US99-04656-15
; Sequence 15, Application PC/TUS9904656
; GENERAL INFORMATION:
; APPLICANT: Basteck, Patrick D.
; APPLICANT: Baumbach, George A.
; APPLICANT: Lang, John M.
; APPLICANT: Carbonell, Ruben G.
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides
; FILE REFERENCE: 017956-000200PC
; CURRENT APPLICATION NUMBER: PCT/US99/04656
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 09/127,574
; EARLIER FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: synthesized on Toyopearl AF Chelate 650 M resin
; OTHER INFORMATION: modified by 4,7,10-trioxa-1,13-tridecanediamine
; OTHER INFORMATION: (Ivotda) and alanine tested for alpha-1
; OTHER INFORMATION: proteinase inhibitor (ALPI) binding
PCT-US99-04656-15

Query Match 57.5%; Score 23; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wry 3
Db 3 WRY 5

RESULT 10
US-08-482-230-124
; Sequence 124, Application US/084822230
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,230
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-230-124

Query Match 57.5%; Score 23; DB 9; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
Db 2 WRWR 5

RESULT 11
US-08-563-128-124
; Sequence 124, Application US/08563128
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.

APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92623-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/563,128
FILING DATE: 29-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP6
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-563-128-124

Query Match 57.5%; Score 23; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 wtyr 4
||:|
Db 2 WRWR 5

RESULT 12
US-08-564-690-124
Sequence 124, Application US/08564690
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgerson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92623-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,690
FILING DATE: 29-NOV-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP5
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-564-690-124

Query Match 57.5%; Score 23; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 wtyr 4
||:|
Db 2 WRWR 5

RESULT 13
US-08-564-693-124
Sequence 124, Application US/08564693
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgerson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92623-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,693
FILING DATE: 29-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP8
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-564-693-124

Query Match 57.5%; Score 23; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
||:|
Db 2 WRWR 5

RESULT 14

US-08-564-765-124
; Sequence 124, Application US/08564765
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,765
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-564-765-124

Query Match 57.5%; Score 23; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
||:|
Db 2 WRWR 5

RESULT 15

US-09-007-288B-54
; Sequence 54, Application US/09007288B
; GENERAL INFORMATION:
; APPLICANT: Fuglsang, Claus Crone
; APPLICANT: Okkels, Jens Sigurd
; APPLICANT: Petersen, Dorte Aaby
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Thellersen, Marianne
; APPLICANT: Svenden, Allan
; APPLICANT: Borch, Kim
; APPLICANT: Royer, John C.

; APPLICANT: Kretzschmar, Titus
; APPLICANT: Halkier, Torben
; APPLICANT: Wind, Jesper
; APPLICANT: Jorgensen, Steen Troels
; TITLE OF INVENTION: Novel Lipolytic Enzymes
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,288B
; FILING DATE: 14-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4455.404-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide addition
US-09-007-288B-54

Query Match 57.5%; Score 23; DB 15; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
||:|
Db 1 WRWR 4

Search completed: November 8, 2000, 07:28:40
Job time: 97 sec

This Page Blank (uspto)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:23:47 ; Search time 12.14 Seconds
(without alignments)
8.284 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues
Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	40	100.0	9	2	US-08-406-330-38
2	40	100.0	9	2	US-08-556-597-38
3	40	100.0	10	2	US-08-406-330-1
4	40	100.0	10	2	US-08-556-597-1
5	34	85.0	10	2	US-08-406-330-4
6	34	85.0	10	2	US-08-556-597-4
7	33	82.5	42	3	US-08-924-330A-3
8	33	82.5	42	3	US-08-924-330A-4
9	33	82.5	423	3	US-08-955-713-2
10	33	82.5	469	3	US-08-704-711A-16
11	33	82.5	476	2	US-08-955-713-4
12	32	80.0	10	2	US-08-406-330-3
13	32	80.0	10	2	US-08-406-330-6
14	32	80.0	10	2	US-08-556-597-3
15	32	80.0	10	2	US-08-556-597-6
16	32	80.0	337	1	US-08-312-387B-5
17	32	80.0	337	1	US-08-312-387B-12
18	32	80.0	337	1	US-08-683-426-5
19	32	80.0	337	1	US-08-683-426-12
20	32	80.0	337	1	US-08-683-458-5
21	32	80.0	337	1	US-08-683-458-12
22	32	80.0	337	2	US-08-878-360-5
23	32	80.0	337	2	US-08-878-360-12
24	32	80.0	483	3	US-08-369-822C-22
25	32	80.0	483	3	US-08-369-822C-37
26	32	80.0	483	3	US-08-434-831B-34
27	31	77.5	10	2	US-08-406-330-5
28	31	77.5	10	2	US-08-556-597-5

Sequence 35, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 1, Appl
Sequence 49, Appl
Sequence 2, Appl
Patent No. 5472691
Sequence 45, Appl
Sequence 53, Appl
Patent No. 5472691

ALIGNMENTS

RESULT 1
US-08-406-330-38
Sequence 38, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/406,330
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-38

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wryrey 6
Db 3 WRYREY 8

RESULT
US-08-556-597-38
; Sequence 38, Application US/08556597
; Patent No. 587155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; NAME: Timian, Susan J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-38

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
DB 3 WRYREY 8

RESULT
US-08-406-330-1
; Sequence 1, Application US/08406330
; Patent No. 581748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-1

Query Match 100.0%; Score 40; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
DB 4-WRYREY 9

RESULT
US-08-566-597-1
; Sequence 1, Application US/08556597
; Patent No. 587155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-1

Query Match 100.0%; Score 40; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 4 WRYREY 9

RESULT 5
US-08-406-330-4
; Sequence 4, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-4

Query Match 100.0%; Score 40; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 4 WRYREY 9

RESULT 6
US-08-556-597-4
; Sequence 4, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-4

Query Match 85.0%; Score 34; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.81;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 4 WRYSEY 9

RESULT 7
US-08-924-330A-3
; Sequence 3, Application US/08924330A
; Patent No. 6022948
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 6022948th Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:

; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-4

Query Match 85.0%; Score 34; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.81;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 4 WRYSEY 9

RESULT 7
US-08-924-330A-3
; Sequence 3, Application US/08924330A
; Patent No. 6022948
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 6022948th Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/924,330A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,226
; FILING DATE: 17-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-330A-3

Query Match 82.5%; Score 33; DB 3; Length 42;
Best Local Similarity 83.3%; Pred. No. 4.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
||| ||
Db 17 WRYDEY 22

RESULT 8
US-08-924-330A-4
; Sequence 4, Application US/08924330A
; Patent No. 6022948
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 6022948th Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,330A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,226
; FILING DATE: 17-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-330A-4

Query Match 82.5%; Score 33; DB 3; Length 42;
Best Local Similarity 83.3%; Pred. No. 4.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
||| ||
Db 17 WRYDEY 22

RESULT 9
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5955308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMAN, DERR
; APPLICANT: HALSEY, WENDY
; TITLE OF INVENTION: CDNA CLONE HECAD54 THAT ENCODES A HUMAN 7-TRANS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-955-713-2

Query Match 82.5%; Score 33; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryre 5
|||||
Db 392 WRYRE 396

RESULT 10
US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd

;; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
;; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/704,711A
;; FILING DATE: 20-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/DE95/00357
;; FILING DATE: 17-MAR-1995
;; PRIOR APPLICATION DATA: DE 4438838.1
;; FILING DATE: 21-OCT-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: DE 4409663.1
;; FILING DATE: 17-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GRANADOS, Patricia D.
;; REGISTRATION NUMBER: 33,683
;; REFERENCE/DOCKET NUMBER: 26083/124
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 469 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-704-711A-16

Query Match 82.5%; Score 33; DB 3; Length 469;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryyre 6
||| ||
Db 398 WRYDEY 403

RESULT 11
US-08-955-713-4
;; Sequence 4, Application US/089555713
;; Patent No. 5953308
;; GENERAL INFORMATION:
;; APPLICANT: SATHE, GANESH
;; APPLICANT: MOONEY, JEFFREY
;; APPLICANT: BERGSMAN, DEREK
;; APPLICANT: HALSEY, WENDY
;; TITLE OF INVENTION: CDNA CLONE HEAD54 THAT ENCODES
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: RATNER & PRESTIA
;; STREET: P.O. BOX 980
;; CITY: VALLEY FORGE
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19482
;; COMPUTER READABLE FORM:
;; A HUMAN 7-TRANS

;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/955,713
;; FILING DATE: 23-OCT-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/050,124
;; FILING DATE: 18-JUN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PRESTIA, PAUL F
;; REGISTRATION NUMBER: 23,031
;; REFERENCE/DOCKET NUMBER: GH-70087
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-407-0700
;; TELEFAX: 610-407-0701
;; TELEX: 846169
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 476 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-955-713-4

Query Match 82.5%; Score 33; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryyre 5
|||||
Db 303 WRYRE 307

RESULT 12
US-08-406-330-3
;; Sequence 3, Application US/08406330
;; Patent No. 5817748
;; GENERAL INFORMATION:
;; APPLICANT: Miller, Jonathan L.
;; APPLICANT: Lytle, Vicki A.
;; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
;; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
;; NUMBER OF SEQUENCES: 81
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
;; STREET: Clinton Square, P.O. Box 1051
;; CITY: Rochester
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 14603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/406,330
;; FILING DATE:
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Timian, Susan J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20884/100
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1636
;; TELEFAX: (716) 263-1600
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-3

Query Match 80.0%; Score 32; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 4 WRYFEY 9

RESULT 13
US-08-406-330-6
; Sequence 6, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-6

Query Match 80.0%; Score 32; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 1 WRQREY 6

RESULT 14
US-08-556-597-3
; Sequence 3, Application US/08556597
; Patent No. 5877155

;
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-3

Query Match 80.0%; Score 32; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 4 WRYFEY 9

RESULT 15
US-08-556-597-6
; Sequence 6, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/556,597
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/406,330
;; FILING DATE: 17-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Timlan, Susan J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20884/101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1636
;; TELEFAX: (716) 263-1600
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-556-597-6

Query Match 80.0%; Score 32; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
|||
Db 1 WRQREY 6

Search completed: November 8, 2000, 07:25:38
Job time: 111 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:23:23 ; Search time 15.08 Seconds
(without alignments)
13.605 Million cell updates/sec

Title: 09-258947-1

Perfect score: 40

Sequence: 1 wryrey 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.*
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6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.*
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18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	9	18	Human platelet gly
2	40	100.0	9	19	Mimotope capable o
3	40	100.0	10	18	Human platelet gly
4	40	100.0	10	19	Mimotope capable o
5	37	92.5	254	20	Mistletoe lectin A
6	37	92.5	254	20	Mistletoe lectin A
7	34	85.0	10	18	Human platelet gly
8	34	85.0	10	19	Mimotope capable o
9	33	82.5	42	19	Pig CII TMP-2 bind
10	33	82.5	42	19	Human CII TMP-2 bi
11	33	82.5	335	9	DNA polymerase bet
12	33	82.5	370	16	Type I matrix meta

13	33	82.5	423	20	Human 7-transmembr
14	33	82.5	457	10	Sequence of human
15	33	82.5	469	8	Sequence encoded b
16	33	82.5	476	20	Human 7-transmembr
17	33	82.5	513	19	Euphorbia lagascae
18	32	80.0	10	18	Human platelet gly
19	32	80.0	10	18	Human platelet gly
20	32	80.0	10	19	Mimotope capable o
21	32	80.0	10	19	Mimotope capable o
22	32	80.0	337	17	N. gonorrhoeae gly
23	32	80.0	337	18	Lipo-oligosacchari
24	31	77.5	10	18	Human platelet gly
25	31	77.5	10	19	Mimotope capable o
26	31	77.5	521	19	Human secreted pro
27	31	77.5	1078	20	Tomato xat1 clone
28	31	77.5	1230	18	Potato tuber solub
29	30	75.0	113	21	TSG-5 polypeptide.
30	30	75.0	256	20	Mistletoe lectin A
31	30	75.0	256	20	Mistletoe lectin A
32	30	75.0	260	20	Amino acid sequenc
33	30	75.0	391	21	Amino acid sequenc
34	30	75.0	391	21	Mortierella sp. de
35	30	75.0	445	19	Neisseria meningit
36	30	75.0	491	21	Neisseria meningit
37	30	75.0	668	21	Neisseria meningit
38	30	75.0	668	21	Neisseria meningit
39	30	75.0	714	20	DS9 protein sequen
40	30	75.0	737	21	Neisseria gonorrhoe
41	30	75.0	737	21	Neisseria meningit
42	30	75.0	737	21	Neisseria meningit
43	30	75.0	2599	21	Neisseria meningit
44	29	72.5	10	18	Human platelet gly
45	29	72.5	10	19	Mimotope capable o

ALIGNMENTS

RESULT 1

W15299

ID W15299 standard; peptide; 9 AA.

XX

AC W15299;

XX

XX 30-JAN-1998 (first entry)

DT

XX Human platelet glycoprotein Ib/IX complex epitope mimotope consensus.

DE

XX Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;

XX monoclonal antibody C-34; anti mimotope; binding site; antibody;

KW platelet adhesion; aggregation; agglutination; von Willebrand factor;

KW anti thrombotic drug; ristocetin.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN W09718236-A1.

XX

PD 22-MAY-1997.

XX

PF 08-NOV-1996; 96WO-US17882.

XX

PR 13-NOV-1995; 95US-556597.

XX

PA (UUNY) UNIV NEW YORK STATE RES FOUND.

XX

PI Lyle VA, Miller JL;

XX

DR WPI; 1997-289227/26.

XX

PT Peptide which mimics human platelet glycoprotein Ib/IX complex

XX epitope - also anti-mimotope molecule capable of binding to the

PT peptide and useful to modulate platelet adhesion, aggregation or

PT agglutination
 PS Claim 4; Page 98; 115pp; English.
 CC The present sequence represents the consensus sequence for a mimotope
 CC which functionally mimics a binding site for a monoclonal antibody (MAB)
 CC which recognises an epitope within the human platelet glycoprotein (gp)
 CC Ib/IX complex. More specifically the MAB is C-34. The mimotope peptide
 CC can be used for raising antibodies, as probes to search for anti-
 CC mimotopes and to neutralise the inhibitory activity of those antibodies
 CC which recognise the epitope which is mimicked by the peptide. Anti-
 CC mimotopes can be used to modulate the adhesion, aggregation or
 CC agglutination of platelets by affecting von Willebrand factor
 CC interaction with the platelets through the gp Ib/IX receptor, e.g. as an
 CC anti-thrombotic drug which inhibits the ristocetin induced aggregation
 CC of platelets.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wryrey 6
 Db 3 wryrey 8
 RESULT 2
 ID W1758 standard; peptide; 9 AA.
 AC W1758;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Mimotope capable of binding to monoclonal antibody C-34 #38.
 XX
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5817748-A.
 XX
 PD 06-OCT-1998.
 XX
 PF 17-MAR-1995; 95US-0406330.
 XX
 PR 17-MAR-1995; 95US-0406330.
 XX
 PA (UYN Y) UNIV NEW YORK STATE RES FOUND.
 XX
 PI Lyle VA, Miller JL;
 XX
 DR WPI; 1998-556458/47.
 XX
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 48; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W1752 to W1832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These

CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 XX mimic platelet epitopes.
 SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
 Db 3 wryrey 8

RESULT 3
 W32624
 ID W32624 standard; peptide; 10 AA.
 AC W32624;
 XX

DT 30-JAN-1998 (first entry)

DE Human platelet glycoprotein Ib/IX complex epitope mimotope.

KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.

XX Synthetic.
 OS Homo sapiens.

PN WO9718236-A1.

XX 22-MAY-1997.

PF 08-NOV-1996; 96WO-US17882.

PR 13-NOV-1995; 95US-0556597.

XX (UYN Y) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;

XX WPI; 1997-289227/26.

DR Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination

PS Claim 3; Page 96; 115pp; English.

XX The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (MAB) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the MAB is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.

XX Sequence 10 AA;

Query Match 100.0%; Score 40; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
 |||||

Db 4 wryrey 9

RESULT 4

W71752
 ID W71752 standard; peptide; 10 AA.

XX AC W71752;

DT 08-DEC-1998 (first entry)

XX DE Mimotope capable of binding to monoclonal antibody C-34 #1.

XX KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 binding site; platelet epitope; neutralise; aggregation; inhibition;
 von Willebrand factor interaction; adhesion; agglutination.

XX OS Synthetic.

OS Homo sapiens.

XX PN US5817748-A.

XX PD 06-OCT-1998.

XX PF 17-MAR-1995; 95US-0406330.

XX PR 17-MAR-1995; 95US-0406330.

XX PA (UUNY) UNIV NEW YORK STATE RES FOUND.

XX PI Lyle VA, Miller JL;

XX WPI; 1998-556458/47.

XX PT Peptides that mimic platelet epitope - and neutralise
 aggregation-inhibiting antibody

XX PS Claim 1; Column 47; 26pp; English.

XX CC The present invention provides peptides which functionally mimic a
 binding site for a monoclonal antibody, where the monoclonal antibody
 recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 to monoclonal antibody C-34. The invention also provides an isolated
 molecule capable of binding the mimotopes, where the molecule can be
 an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
 |||||

Db 4 wryrey 9

RESULT 5

Y25980
 ID Y25980 standard; Protein; 254 AA.

XX AC Y25980;

XX DT 18-OCT-1999 (first entry)

XX DE Mistletoe lectin A1 protein fragment.

XX KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin A1.

XX OS Viscum album.

XX PN DE19804210-A1.

XX PD 12-AUG-1999.

XX PF 03-FEB-1998; 98DE-1004210.

XX PR 03-FEB-1998; 98DE-1004210.

XX PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX PI Morris P, Stiefel T, Voelter W, Welters P;

XX WPI; 1999-445335/38.

XX DR N-PSDB; 209104.

XX PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 XX PS Disclosure; Fig 2B; 78pp; German.

XX CC This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MIA)
 of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of the mistletoe lectin A1 protein.

XX SQ Sequence 254 AA;

Query Match 92.5%; Score 37; DB 20; Length 254;
 Best Local Similarity 83.3%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
 |||||

Db 174 wryrqy 179

RESULT 6

Y25983
 ID Y25983 standard; Protein; 254 AA.

XX AC Y25983;

XX DT 18-OCT-1999 (first entry)

```

XX DE Mistletoe lectin A1 (variant) protein fragment.
XX KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
XX KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX KW cancer; cytotoxicity; antigen; isoform; lectin A1.
XX OS Viscum album.
XX PN DE19804210-A1.
XX PD 12-AUG-1999.
XX PF 03-FEB-1998; 98DE-1004210.
XX PR 03-FEB-1998; 98DE-1004210.
XX PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX PI Morris P, Stiefel T, Voelter W, Welters P;
XX DR WPI; 1999-445335/38.
XX DR N-PSDB; Z09107.
XX PT Preparation of mistletoe lectins in heterologous systems,
XX PT particularly for use as anticancer agents and immunostimulants
XX PS Disclosure; Fig 5B; 78pp; German.
XX CC This invention describes a novel mistletoe lectin (I) and its fragments
XX CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
XX CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX CC fragments are used to treat uncontrolled cell growth (particularly
XX CC cancers) and if they lack cytotoxicity, to increase the strength of the
XX CC immune response, particularly to a co-administered antigen
XX CC (tumour-associated, bacterial or viral). The method allows production of
XX CC mistletoe lectin, and its individual chains, in many different isoforms
XX CC and on a large scale, at any time of the year. Recombinant products are
XX CC free from toxins present in natural mistletoe extracts. This sequence
XX CC represents a fragment of a mistletoe lectin A1 protein variant.
XX SQ Sequence 254 AA;

Query Match 92.5%; Score 37; DB 20; Length 254;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
Db 174 wryrdy 179

RESULT 7
W32627
ID W32627 standard; peptide; 10 AA.
XX AC W32627;
XX DT 30-JAN-1998 (first entry)
XX DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
XX KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
XX KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
XX KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
XX KW anti thrombotic drug; ristocetin.
XX OS Synthetic.
XX OS Homo sapiens.

Query Match 85.0%; Score 34; DB 18; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
Db 4 wrysey 9

RESULT 8
W71754
ID W71754 standard; peptide; 10 AA.
XX AC W71754;
XX DT 08-DEC-1998 (first entry)
XX DE Mimotope capable of binding to monoclonal antibody C-34 #4.
XX KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
XX KW binding site; platelet epitope; neutralise; aggregation; inhibition;
XX KW von Willebrand factor interaction; adhesion; agglutination.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5817748-A.
XX PD 06-OCT-1998.
XX PF 17-MAR-1995; 95US-0406330.
XX PR 17-MAR-1995; 95US-0406330.
XX PA (UYNV ) UNIV NEW YORK STATE RES FOUND.
XX OS Synthetic.
XX OS Homo sapiens.

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XX PN WO9718236-A1.
XX PD 22-MAY-1997.
XX PF 08-NOV-1996; 96WO-US17882.
XX PR 13-NOV-1995; 95US-0556597.
XX PA (UYNV ) UNIV NEW YORK STATE RES FOUND.
XX PI Lyle VA, Miller JL;
XX DR WPI; 1997-289227/26.
XX PT Peptide which mimics human platelet glycoprotein Ib/IX complex
XX PT epitope - also anti-mimotope molecule capable of binding to the
XX PT peptide and useful to modulate platelet adhesion, aggregation or
XX PT agglutination
XX PS Claim 3; Page 96; 115pp; English.
XX CC The present sequence represents a mimotope which functionally mimics a
XX CC binding site for a monoclonal antibody (MAB) which recognises an epitope
XX CC within the human platelet glycoprotein (gp) Ib/IX complex. More
XX CC specifically the MAB is C-34. The mimotope peptide can be used for
XX CC raising antibodies, as probes to search for anti-mimotopes and to
XX CC neutralise the inhibitory activity of those antibodies which recognise
XX CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
XX CC to modulate the adhesion, aggregation or agglutination of platelets by
XX CC affecting von Willebrand factor interaction with the platelets through
XX CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
XX CC the ristocetin induced aggregation of platelets.
XX SQ Sequence 10 AA;

Query Match 85.0%; Score 34; DB 18; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
Db 4 wrysey 9

RESULT 8
W71754
ID W71754 standard; peptide; 10 AA.
XX AC W71754;
XX DT 08-DEC-1998 (first entry)
XX DE Mimotope capable of binding to monoclonal antibody C-34 #4.
XX KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
XX KW binding site; platelet epitope; neutralise; aggregation; inhibition;
XX KW von Willebrand factor interaction; adhesion; agglutination.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5817748-A.
XX PD 06-OCT-1998.
XX PF 17-MAR-1995; 95US-0406330.
XX PR 17-MAR-1995; 95US-0406330.
XX PA (UYNV ) UNIV NEW YORK STATE RES FOUND.
XX OS Synthetic.
XX OS Homo sapiens.

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PI Lyle VA, Miller JL;

XX WPI; 1998-556458/47.

XX Peptides that mimic platelet epitope - and neutralise

PT aggregation-inhibiting antibody

XX Claim 1; Column 47; 26pp; English.

XX The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W1752 to W1832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.

XX Sequence 10 AA;

Query Match 85.0%; Score 34; DB 19; Length 10;

Best Local Similarity 83.3%; Pred. No. 1.6;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6

DB 4 wrysey 9

RESULT 9

W59181 W59181 standard; peptide; 42 AA.

XX AC W59181;

XX DT 14-AUG-1998 (first entry)

XX DE Plg CLI TMP-2 binding peptide beta-propeller blade III region.

XX KW Gelatinase A; Gela; TIMP-2; matrix metalloprotease; MMP; beta-propeller;
 KW cell surface activation; inhibition; screening; target; treatment;
 KW disease; tissue repair; tissue damage; rheumatoid arthritis; restenosis;
 KW osteoarthritis.

XX OS Sus scrofa.

XX PN WO9812309-A2.

XX PD 26-MAR-1998.

XX PF 15-SEP-1997; 97WO-US16216.

XX PR 17-SEP-1996; 96US-0026226.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Goldberg GI;

XX DR WPI; 1998-217253/19.

XX Identifying matrix metallo:protease inhibitors - using a target area
 PT comprising specific residues of the TIMP-2 binding site of the
 PT gelatinase-A C-terminal domain

XX

PS Disclosure; Fig 5; 54pp; English.

XX W59179-W59196 are peptide fragments of beta-propeller blade regions
 CC III and IV from C-terminal domains of various matrix metalloprotease
 CC family members which are used in a method to study cell surface
 CC activation and inhibition. The method involves the interaction of an
 CC inhibitor of matrix metalloprotease, TIMP-2 with the enzyme gelatinase A
 CC (Gela). A target area for screening matrix metalloprotease (MMP)
 CC inhibitors comprises the following residues of the TIMP-2 binding site
 CC on the surface of the gelatinase-A (Gela)-C-terminal domain (CTD):
 CC Asp656, Gly651, Phe650 and Tyr636. Also claimed is a target area for
 CC screening MMP inhibitors comprising the following residues of the
 CC TIMP-2 binding site on the surface of the Gela-CTD domain: Asp656,
 CC Gly651, Phe650, Tyr636, Asp615, Lys646, Lys576, Trp574, Arg590, Lys579,
 CC Lys604 and Asn611. The target areas can be used for obtaining MMP
 CC inhibitors which can be used for the treatment of diseases that involve
 CC tissue repair and damage and other diseases in which MMPs are implicated
 CC e.g. rheumatoid arthritis, osteoarthritis and restenosis.

XX Sequence 42 AA;

Query Match 82.5%; Score 33; DB 19; Length 42;

Best Local Similarity 83.3%; Pred. No. 9.7;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6

DB 17 wrydey 22

RESULT 10

W59182 W59182 standard; peptide; 42 AA.

XX AC W59182;

XX DT 14-AUG-1998 (first entry)

XX DE Human CLI TMP-2 binding peptide beta-propeller blade III region.

XX KW Gelatinase A; Gela; TIMP-2; matrix metalloprotease; MMP; beta-propeller;
 KW cell surface activation; inhibition; screening; target; treatment;
 KW disease; tissue repair; tissue damage; rheumatoid arthritis; restenosis;
 KW osteoarthritis.

XX OS Homo sapiens.

XX PN WO9812309-A2.

XX PD 26-MAR-1998.

XX PF 15-SEP-1997; 97WO-US16216.

XX PR 17-SEP-1996; 96US-0026226.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Goldberg GI;

XX DR WPI; 1998-217253/19.

XX Identifying matrix metallo:protease inhibitors - using a target area
 PT comprising specific residues of the TIMP-2 binding site of the
 PT gelatinase-A C-terminal domain

PS Disclosure; Fig 5; 54pp; English.

XX W59179-W59196 are peptide fragments of beta-propeller blade regions
 CC III and IV from C-terminal domains of various matrix metalloprotease
 CC family members which are used in a method to study cell surface
 CC activation and inhibition. The method involves the interaction of an
 CC inhibitor of matrix metalloprotease, TIMP-2 with the enzyme gelatinase A

CC (Gela). A target area for screening matrix metalloprotease (MMP)
 CC inhibitors comprises the following residues of the TIMP-2 binding site
 CC on the surface of the gelatinase-A (Gela)-C-terminal domain (CTD):
 CC Asp656, Gly651, Phe650 and Tyr636. Also claimed is a target area for
 CC screening MMP inhibitors comprising the following residues of the
 CC TIMP-2 binding site on the surface of the Gela-CTD domain: Asp656,
 CC Gly651, Phe650, Tyr636, Asp615, Lys646, Lys576, Trp574, Arg590, Lys579,
 CC Lys604 and Asn611. The target areas can be used for obtaining MMP
 CC inhibitors which can be used for the treatment of diseases that involve
 CC tissue repair and damage and other diseases in which MMPs are implicated
 CC e.g. rheumatoid arthritis, osteoarthritis and restenosis.
 XX
 SQ Sequence 42 AA;

Query Match 82.5%; Score 33; DB 19; Length 42;
 Best Local Similarity 83.3%; Pred. No. 9.7;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
 ||| ||
 Db 17 wrydey 22

RESULT 11
 P80386
 ID P80386 standard; protein; 335 AA.
 XX
 AC P80386;
 XX
 DT 19-NOV-1990 (first entry)
 XX
 DE DNA polymerase beta lacking nuclease activity.
 XX
 KW mammalian DNA polymerase beta subunit; pUC118+P'+S;
 KW E.coli Jmpbeta5.
 XX
 OS Rattus rattus.
 XX
 PN W08804321-A.
 XX
 PD 16-JUN-1988.
 XX
 PF 03-DEC-1987; 87WO-JP00938.
 XX
 PR 03-DEC-1987; 87JP-0288371.
 XX
 PA (MITK) MITSUI TOATSU CHEM INC.
 XX
 PI Matsukage A, Yamaguchi M, Date T;
 XX
 DR WPI; 1988-175469/25.
 DR N-PSDB; N80393.
 XX

PT DNA polymerase without nuclease activity -
 PT obtd by culture of transformant E.coli incorporating DNA coding for
 PT DNA polymerase beta of mammalian origin.
 XX

PS Claim 1; Page 46; 65pp; Japanese.
 XX
 CC DNA coding for the N-terminal of rat DNA polymerase beta subunit
 CC contained in pUC9-10F was cloned into pUC118 to give plasmid
 CC pUC188+F. A short region of beta-gal sequence is excised to leave
 CC pUC118+F'. This is coupled to plasmid pUC9-10S which encodes the
 CC C-terminal region of rat DNA pol beta. The resultant plasmid
 CC (pUC118+F'+S) contains the entire coding sequence and is used to
 CC transform E.coli JMI09. Transformant hosts are denoted Jmpbetas.
 CC The protein can be expressed in high yield and is therefore readily
 CC purified. It is useful for genetic engineering due to its lack of
 CC nuclease activity.
 XX
 SQ Sequence 335 AA;

Query Match 82.5%; Score 33; DB 9; Length 335;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryre 5
 |||||
 Db 325 wryre 329

RESULT 12
 R87016
 ID R87016 standard; Protein; 370 AA.
 XX
 AC R87016;
 XX
 DT 19-MAR-1996 (first entry)
 XX
 DE Type I matrix metalloprotease.
 XX
 KW Type I matrix metalloprotease; MMP-I; collagenase; nematode;
 KW disease resistance; transgenic plant; crop improvement;
 KW nematocide; biological control; potato; Solanum tuberosum.
 XX
 OS Not specified.
 XX
 PN W09530017-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 26-APR-1995; 95WO-GB00944.
 XX
 PR 29-APR-1994; 94EP-0303168.
 XX
 PA (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 XX
 PI Shields R, Stratford R;
 XX
 DR WPI; 1995-393088/50.
 DR N-PSDB; T07301.
 XX

PT Nucleic acid for increasing plant resistance to nematodes - encodes
 PT a polypeptide with collagenase activity.
 XX

PS Example; Page 23-24; 41pp; English.
 XX

CC The mature form of type I matrix metalloprotease (MMP-I) (R87016)
 CC has collagenase activity that degrades native collagens types I,
 CC II and III. DNA (T07301) coding for mature MMP-I was modified
 CC for expression in plants by addition of a start codon and a patatin
 CC leader sequence. Transgenic potato cv. Desiree and Maris Piper
 CC plants were obtd. that showed high levels of resistance to the
 CC nematode Globodera pallida.
 XX

SQ Sequence 370 AA;

Query Match 82.5%; Score 33; DB 16; Length 370;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
 |||||
 Db 299 wrydey 304

RESULT 13
 W88460
 ID W88460 standard; Protein; 423 AA.
 XX
 AC W88460;
 XX

DT 10-MAY-1999 (first entry)
 XX Human 7-transmembrane receptor HE0AD54.
 XX
 XX HE0AD54; 7-transmembrane receptor; G protein coupled receptor;
 KW signal transduction; human; infection; HIV-1; HIV-2; pain; cancer;
 KW anorexia; bulimia; aschma; parkinson's disease; hypotension;
 KW hypertension; acute heart failure; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; ulcer; allergy;
 KW benign prostatic hypertrophy; anxiety; schizophrenia; delirium;
 KW manic depression; dementia; severe mental retardation; dyskinesia;
 KW Huntington's disease; Gilles de la Tourette's syndrome; diagnosis;
 KW therapy; vaccine.
 XX
 XX Homo sapiens.
 XX
 XX EP892051-A2.
 XX
 XX 20-JAN-1999.
 XX
 XX 27-MAY-1998; 98EP-0304192.
 XX
 XX 23-OCT-1997; 97US-0955713.
 PR 18-JUN-1997; 97US-0060124.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Bergsma DJ, Halsey WS, Mooney JL, Sathe GM;
 XX WPI; 1999-083568/08.
 DR N-PSDB; X06947.
 XX
 XX New G-protein coupled receptor (HE0AD54) polypeptide and
 PT polynucleotide - useful as diagnostic reagents, and for prevention
 PT and treatment of HIV infections and cancer
 XX
 XX Claim 11; Page 20-21; 25pp; English.
 XX
 XX This is the amino acid sequence of a novel human G protein coupled
 CC receptor, designated HE0AD54, as deduced from a cDNA clone (see
 CC X06947) isolated from an eosinophil library. A method is claimed
 CC for diagnosing susceptibility to disease resulting from mutation of
 CC the HE0AD54 gene or imbalance in HE0AD54 polypeptide expression
 CC levels. HE0AD54 agonists/antagonists can be used to activate/inhibit
 CC HE0AD54 activity. Direct administration of antisense sequences is
 CC used to prevent expression, while administration of HE0AD54 is used
 CC to treat conditions associated with a lack of HE0AD54 protein. Gene
 CC therapy may also be used to affect endogenous HE0AD54 polypeptide
 CC expression. HE0AD54 polypeptides can be administered directly or
 CC as a vaccine to inoculate against disease. Diseases diagnosed,
 CC prevented and treated include bacterial, fungal, protozoan and
 CC viral infections, particularly HIV-1 or HIV-2 infections, pain,
 CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute
 CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, angina pectoris, myocardial infarction, ulcer,
 CC allergy, benign prostatic hypertrophy, and psychotic and
 CC neurological disorders including anxiety, schizophrenia, manic
 CC depression, delirium, dementia, severe mental retardation and
 CC dyskinesias, such as Huntington's disease or Gilles de la
 CC Tourette's syndrome.
 XX
 XX Sequence 423 AA;
 XX
 XX Query Match 82.5%; Score 33; DB 20; Length 423;
 XX Best Local Similarity 100.0%; Pred. No. 91;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 wryre 5
 XX |||||
 Db 392 wryre 396
 XX

RESULT 14
 P93628
 ID P93628 standard; Protein; 457 AA.
 XX
 AC P93628;
 XX
 DT 19-AUG-1991 (first entry)
 XX
 XX Sequence of human interstitial procollagenase.
 DE
 XX Hypertrophic scar; keloid; intervertebral disc disease; enzyme.
 KW
 XX Homo sapiens.
 XX OS
 XX GB2209526-A.
 PN
 XX 17-MAY-1989.
 PD
 XX 02-SEP-1988; 88GB-0020803.
 XX PF
 XX 04-SEP-1987; 87US-0093421.
 XX PR
 XX (UNIW) UNIV OF WASHINGTON.
 XX PA
 XX Eisen AZ, Goldberg GI;
 XX PI
 XX WPI; 1989-147011/20.
 XX DR
 XX DNA encoding human type IV collagenase (gelatinase) - for use in the
 PT treatment of hypertrophic scars, keloids and intervertebral disc
 PT disease
 XX
 XX Example; Fig 6; 36pp; English.
 PS
 XX The original source of the protein material was H-ra's transformed
 CC human bronchial epithelial cells (rBE-1). The AA sequence was then
 CC used to develop oligonucleotide probes which were used to screen a
 CC cDNA library of human skin fibroblast mRNA. The longest clone, pGEL
 CC 186.2, represented almost the full gelatinase mRNA sequence except
 CC the leader sequence encoding the first few AA's of the signal
 CC peptide. Figure 6 compares the SOS of human type IV procollagenase
 CC P96143), human prostromelysin (P93629), human interstitial
 CC procollagenase (P93628) and rat transin (P93630).
 XX
 SQ Sequence 457 AA;
 XX
 XX Query Match 82.5%; Score 33; DB 10; Length 457;
 XX Best Local Similarity 83.3%; Pred. No. 99;
 XX Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Qy 1 wryre 6
 Db 386 wrydey 391
 XX
 XX
 XX P70611;
 AC
 XX
 XX 15-APR-1991 (first entry)
 DT
 XX Sequence encoded by human skin collagenase cDNA.
 DE
 XX Enzyme; protease.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Cleavage-site 19..20
 FT /note= "putative site of the signal peptide
 FT

FT Modified-site 120..122 cleavage"
FT /note= "potential N-glycosylation site"
FT Modified-site 141..143
FT /note= "see above"
FT Misc-difference 101
FT /note= "NH2-terminus of the proteolytically
FT activated enzyme form"
XX
XX GB2182665-A.
XX
XX 20-MAY-1987.
XX
XX 11-NOV-1986; 86GB-0026914.
XX
XX 12-NOV-1985; 85US-0797262.
XX
XX (MONS) MONSANTO CO.
XX (UNIW) UNIV OF WASHINGTON.
XX
XX Eisen AZ, Goldberg GI, Bauer EA;
XX
XX WPI: 1987-137944/20.
XX N-PSDB; N70959.
XX
XX New human skin fibroblast collagenase - is obtd. by recombinant
XX dna procedures for treating hypertrophic scars, keloids and
XX intervertebral disc disease
XX
XX Claim 3: Fig 2; 10pp; English.
XX
XX Cytoplasmic RNA was prepd. by using normal adult human skin
XX fibroblasts to give conditioned medium, and procollagenase was
XX purified. Protein sequencing, primer extension reaction and
XX construction of a cDNA library were carried out. Human skin
XX fibroblast protein is pref. glycosylated at Asn 120 and Asn 143.
SQ Sequence 469 AA;

Query Match 82.5%; Score 33; DB 8; Length 469;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 wryrey 6
DB 398 wrydey 403

Search completed: November 8, 2000, 07:25:22
Job time: 119 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:24:07 ; Search time 13.37 Seconds
(without alignments)
28.479 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues
Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37	92.5	254	2	PD0018	mistletoe lectin I
2	36	90.0	404	2	G69318	threonine synthase
3	36	90.0	406	2	G69131	threonine synthase
4	36	90.0	642	2	H70331	ATP-dependent heli
5	35	87.5	169	2	A64396	hypothetical prote
6	35	87.5	329	1	D71316	conserved hypothet
7	33	82.5	250	2	H75355	hypothetical prote
8	33	82.5	276	2	S74745	ABC-type transport
9	33	82.5	335	2	A27112	DNA-directed DNA p
10	33	82.5	405	2	H64482	threonine synthase
11	33	82.5	468	1	KCRBI	interstitial colla
12	33	82.5	469	1	KCHUI	interstitial colla
13	33	82.5	469	1	KCPGI	interstitial colla
14	33	82.5	469	1	KCBOI	interstitial colla
15	33	82.5	517	2	A71707	lipopolysaccharide
16	33	82.5	635	2	S74718	sulfite reductase
17	33	82.5	641	2	S69651	SAC2 protein - yea
18	33	82.5	831	2	A48489	nitrate reductase
19	33	82.5	831	2	S50163	nitrate reductase
20	33	82.5	986	2	S49394	HsdR1 protein - My
21	33	82.5	997	2	S67697	probable membrane
22	32	80.0	229	2	S42376	hypothetical prote
23	32	80.0	315	2	A47269	transcription regu
24	32	80.0	661	2	T15802	hypothetical prote
25	32	80.0	665	2	T15801	hypothetical prote
26	32	80.0	783	2	T30644	hypothetical prote
27	32	80.0	2109	1	ZLVNNU	genome polyprotein
28	32	80.0	2109	1	A46309	genome polyprotein
29	31	77.5	174	2	A70337	hypothetical prote

30	31	77.5	443	2	G75038	probable na+/h+ an
31	31	77.5	454	2	G70476	conserved hypothet
32	31	77.5	567	2	T40057	probable single-st
33	31	77.5	594	2	T31744	hypothetical prote
34	31	77.5	649	2	T32755	hypothetical prote
35	31	77.5	729	2	T06797	probable 1,4-alpha
36	31	77.5	1230	2	T07663	soluble starch syn
37	30	75.0	70	2	S10664	hypothetical prote
38	30	75.0	74	2	B71282	hypothetical prote
39	30	75.0	166	2	B70613	hypothetical prote
40	30	75.0	185	2	F64049	CDPdiacylglycerol-
41	30	75.0	240	2	G70303	cytochrome c - Aqu
42	30	75.0	243	2	B69951	hypothetical prote
43	30	75.0	256	2	T37048	probable nitrate r
44	30	75.0	264	2	I40184	hypothetical prote
45	30	75.0	285	2	T36296	hypothetical prote

ALIGNMENTS

RESULT 1
PD0018
mistletoe lectin I A chain - Viscum album (fragment)
C:Species: Viscum album
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
C:Accession: PD0018
R:Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A:Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum a
A:Reference number: PD0018; MUID:98308123
A:Accession: PD0018
A:Molecule type: protein
A:Residues: 1-254 <ESC>
C:Superfamily: ricin; rRNA N-glycosidase homology
F.7-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 92.5%; Score 37; DB 2; Length 254;
Best Local Similarity 83.3%; Pred. No. 3.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 174 WRYRQY 179
|||||

RESULT 2
G69318
threonine synthase (EC 4.2.99.2) thrC-1 AF0551 [similarity] - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-May-2000
C:Accession: G69318
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Klrkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: G69318
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-404 <KLE>
A:Cross-references: GB:AE001066; GB:AE000782; NID:g2689389; PIDN:AAB90683.1; PID:g265
C:Superfamily: threonine dehydratase
C:Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate
F.107/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 9.5;

Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1 wryrey 6								
Db	56 WYREF 61								
RESULT	3								
G69131	threonine synthase (EC 4.2.99.2) - Methanobacterium thermoautotrophicum								
C:Species:	Methanobacterium thermoautotrophicum								
C>Date:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999								
C:Accession:	G69131								
R:Smith, D.R.;	Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;								
;	Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, M.								
kl, S.;	Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.								
J. bacteriol.	179, 7135-7155, 1997								
A:Title:	Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct								
A:Reference number:	A69000; MUID:98037514								
A:Accession:	G69131								
A:Status:	preliminary; nucleic acid sequence not shown; translation not shown								
A:Molecule type:	DNA								
A:Residues:	1-406 <MTH>								
A:Cross-references:	GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84759.1; PID:g262130								
A:Experimental source:	strain Delta H								
C:Genetics:									
A:Note:	MTH253								
C:Function:									
A:Description:	catalyzes hydrolyzation of O-phospho-L-homoserine to L-threonine and orth								
A:Pathway:	threonine biosynthesis								
A:Note:	pyridoxal phosphate cofactor								
C:Superfamily:	threonine dehydratase								
C:Keywords:	carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate; threonine biosynth								
F:104/Binding site:	pyridoxal phosphate (Lys) (covalent) #status predicted								
Query Match	90.0%;	Score	36;	DB	2;	Length	406;		
Best Local Similarity	83.3%;	Pred. No.	9.5;						
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1 wryrey 6								
Db	53 WYREF 58								
RESULT	4								
H70331	Atp-dependent helicase (DinG family) - Aquifex aeolicus								
C:Species:	Aquifex aeolicus								
C>Date:	08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999								
C:Accession:	H70331								
R:Deckert, G.;	Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov								
V.									
Nature	392, 353-358, 1998								
A:Title:	The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.								
A:Reference number:	A70300; MUID:98196666								
A:Accession:	H70331								
A:Status:	preliminary; nucleic acid sequence not shown; translation not shown								
A:Molecule type:	DNA								
A:Residues:	1-642 <AQF>								
A:Cross-references:	GB:AE000685; NID:g2983026; PIDN:AAC06640.1; PID:g2983030; GB:AE00065								
A:Experimental source:	strain VF5								
C:Genetics:									
A:Gene:	ding								
Query Match	90.0%;	Score	36;	DB	2;	Length	642;		
Best Local Similarity	83.3%;	Pred. No.	15;						
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1 wryrey 6								
Db	611 WYREF 616								

RESULT 5
A64396
hypothetical protein MJ0769 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: A64396
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: A64396
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-169 <BUL>
A:Cross-references: GB:U67522; GB:L77117; NID:gl591473; PIDN:AAB98774.1; PID:gl499589
C:Genetics:
A:Map position: REV690989-690480

Query Match 87.5%; Score 35; DB 2; Length 169;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 wryrey 6
|
|
|
|
Db 121 WEYREY 126
RESULT 6
D71316
conserved hypothetical protein TP0496 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: D71316
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: D71316
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-329 <COL>
A:Cross-references: GB:AE001226; GB:AE000520; NID:g3322785; PID:g3322786
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0496
C:Superfamily: hypothetical protein BB0714; tetratricopeptide repeat homology

Query Match 87.5%; Score 35; DB 1; Length 329;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 wryrey 6
|
|
|
|
Db 57 WYREY 62
RESULT 7
H75355
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: H75355
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;

S.: Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: H75355

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-250 <WHI>

A:Cross-references: GB:AB002018; GB:AE000513; NID:g6459537; PIDN:AAE11325.1; PID:g645954

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1763

A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 250;

Best Local Similarity 66.7%; Pred. No. 23;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6

|||||

Db 196 WRFEDY 201

RESULT 8

S74745 ABC-type transport protein slr0977 - Synecocystis sp. (strain PCC 6803)

N:Alternate names: protein slr0977

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S74745

O: Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, M.;

R: K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

s.

A:Reference number: S74322; MUID:97061201

A:Accession: S74745

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-276 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:gl651897; PIDN:BAAL6896.1; PID:g165197

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: Integral membrane O-antigen translocator protein rfbA

C:Keywords: transport protein

Query Match 82.5%; Score 33; DB 2; Length 276;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 5

|||||

Db 24 WRYRE 28

RESULT 9

A27112 DNA-directed DNA polymerase (EC 2.7.7.7) beta chain - rat

N:Alternate names: high-molecular-weight DNA polymerase beta

C:Species: Rattus norvegicus (Norway rat)

C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Jun-1999

C:Accession: A27112; A25445; B44465; A44469; A35034; JC5118; I84482; A29405

R: Matsukage, A.; Nishikawa, K.; Ooi, T.; Seto, Y.; Yamaguchi, M.

J. Biol. Chem. 262, 8960-8962, 1987

A:Title: Homology between mammalian DNA polymerase beta and terminal deoxynucleotidyltra

A:Reference number: A27112; MUID:87250529

A:Accession: A27112

A:Molecule type: mRNA

A:Residues: 1-335 <MAP>

A:Cross-references: GB:J02776; NID:g206277; PIDN:AAA41901.1; PID:g206278

R:Zmudzka, B.Z.; SenGupta, D.; Matsukage, A.; Cobiachni, F.; Kumar, P.; Wilson, S.H.

Proc. Natl. Acad. Sci. U.S.A. 83, 5106-5110, 1986

A:Title: Structure of rat DNA polymerase beta-revealed by partial amino acid sequenci

A:Reference number: A94107; MUID:86259741

A:Accession: A25445

A:Molecule type: mRNA

A:Residues: 18-335 <ZMU>

A:Cross-references: GB:M13961; NID:g206275; PIDN:AAA41900.1; PID:g206276

A:Note: the authors translated the codon CGT for residue 211 as Leu

R: Casas-Finet, J.R.; Kumar, A.; Karpel, R.L.; Wilson, S.H.

Biochemistry 31, 10272-10280, 1992

A:Title: Mammalian DNA polymerase beta: characterization of a 16-kDa transdomain frag

A:Reference number: A44469; MUID:93041712

A:Accession: B44469

A>Status: preliminary

A:Molecule type: protein

A:Residues: 'X', 85-93 <CAS>

A:Note: sequence extracted from NCBI backbone (NCBIP:116624)

A:Accession: A44469

A>Status: preliminary

A:Molecule type: protein

A:Residues: 19-26, 'X', 28-33 <CA2>

A:Note: sequence extracted from NCBI backbone (NCBIP:116617)

R: Kumar, A.; Widen, S.G.; Williams, K.R.; Kedar, P.; Karpel, R.L.; Wilson, S.H.

J. Biol. Chem. 265, 2124-2131, 1990

A:Title: Studies of the domain structure of mammalian DNA polymerase beta. Identifica

A:Reference number: A35034; MUID:90130463

A:Accession: A35034

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 2-81; 84-113; 128-137; 141-182; 184-200; 210-227; 'L', 229-253; 259-280; 284-324; 3

R: Konopinski, R.; Nowak, R.; Siedlecki, J.A.

Gene 176, 191-195, 1996

A:Title: Alternative polyadenylation of the gene transcripts encoding a rat DNA polym

A:Reference number: JC5118; MUID:97075929

A:Accession: JC5118

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-335 <KON>

A:Cross-references: GB:U38801; NID:gl055329; PIDN:AAB00389.1; PID:gl055330

R: Date, T.; Tanihara, K.; Yamamoto, S.; Nomura, N.; Matsukage, A.

Nucleic Acids Res. 20, 4859-4864, 1992

A:Title: Two regions in human DNA polymerase beta mRNA suppress translation in Escher

A:Accession number: I38366; MUID:93027206

A:Status: translated from GB/EMBL/DDBBJ

A:Molecule type: DNA

A:Residues: 149-202 <RES>

A:Cross-references: EMBL:X68945; NID:g312929; PIDN:CAA48761.1; PID:g938280

C:Genetics:

A:Gene: DNA-pol-beta

C:Superfamily: DNA-directed DNA polymerase beta

C:Keywords: nucleotidyltransferase

Query Match 82.5%; Score 33; DB 2; Length 335;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 5

|||||

Db 325 WRYRE 329

RESULT 10

H64482

threonine synthase (EC 4.2.99.2) - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Jun-1999

C:Accession: H64482

R: Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

erson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
A;Reference number: A64300; MUID:96337999
A;Accession: H64482
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-405 <BUL>
A;Cross-references: GB:067587; GB:L77117; NID:gi592103; PIDN:AAB99473.1; PID:gi1592106; T
C;Genetics:
A;Gene: thrC
A;Map position: REV1435420-1434203
C;Function:
A;Description: catalyzes hydrolyzation of O-phospho-L-homoserine to L-threonine and orth
A;Pathway: threonine biosynthesis
A;Note: pyridoxal phosphate cofactor
C;Superfamily: threonine dehydratase
C;Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate; threonine biosynth
F;106/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 82.5%; Score 33; DB 2; Length 405;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 53 WRYLEY 58

RESULT 11
KCRBI
Interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C;Species: *Oryctolagus cuniculus* (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A27500; B27500; I46694
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote
A;Reference number: A27500; MUID:98077876
A;Accession: A27500
A;Molecule type: mRNA
A;Residues: 1-468 <FIN>
A;Cross-references: GB:M19240
A;Accession: B27500
A;Molecule type: DNA
A;Residues: 1-391;399-468 <PI2>
A;Cross-references: GB:M17820
A;Note: the location of the intron between exons 7 and 8 is approximate
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerhoff
Coll. Relat. Res. 6, 239-248, 1986
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial
A;Reference number: I46694; MUID:87029174
A;Accession: I46694
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 449-468 <FI3>
A;Cross-references: GB:M25663; NID:g531211; PIDN:AAA31203.1; PID:g531212
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th
C;Comment: Procollagenase can be activated without removal of the activation peptide. St
tion peptide by other proteinases.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C;Genetics:
A;Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-468/Product: procollagenase #status predicted <PRO>
F;19-96/Domain: activation peptide #status predicted <ACT>
F;59-260/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory

F;99-468/Product: interstitial collagenase #status predicted <MAT>
F;271-465/Domain: hemopexin repeat homology <PXN>
F;91, 217, 221, 227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #stat
F;119, 142/Binding site: carboxylate (Asn) (covalent) #status predicted
F;217, 221, 227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;277-465/Disulfide bonds: #status predicted

Query Match 82.5%; Score 33; DB 1; Length 468;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 397 WRYDEY 402

RESULT 12
KCHUI
Interstitial collagenase (EC 3.4.24.7) precursor - human
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue
C;Species: *Homo sapiens* (man)
C;Date: 13-Aug-1986 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595;
R;Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-
Cancer Res. 50, 5431-5437, 1990
A;Title: Cloning and characterization of human tumor cell interstitial collagenase.
A;Reference number: A37308; MUID:90352587
A;Accession: A37308
A;Molecule type: mRNA
A;Residues: 1-469 <TEM>
A;Cross-references: GB:X54925; NID:g30125; PIDN:CRA38691.1; PID:g30126
R;Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Finl, M.E.; White, H.D.
J. Clin. Invest. 79, 543-546, 1987
A;Title: Molecular cloning of human synovial cell collagenase and selection of a sing
A;Reference number: S22766; MUID:87109799
A;Accession: S22766
A;Molecule type: DNA
A;Residues: 1-63;65-70 <BRI>
A;Cross-references: EMBL:M15996; NID:gi180666; PIDN:AAA35700.1; PID:gi180667
R;Angel, P.; Baumann, I.; Stein, B.; Dellus, H.; Rahmsdorf, H.J.; Herrlich, P.
Mol. Cell. Biol. 7, 2256-2266, 1987
A;Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gen
A;Reference number: I57620; MUID:87257941
A;Accession: I57620
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-35 <RES>
A;Cross-references: GB:M16567; NID:gi180668; PIDN:AAA52033.1; PID:gi180669
R;Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Elsen, A.Z
J. Biol. Chem. 261, 6600-6605, 1986
A;Title: Human fibroblast collagenase. Complete primary structure and homology to an
A;Reference number: A00996; MUID:86196089
A;Accession: A00996
A;Molecule type: mRNA
A;Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>
A;Cross-references: GB:M13509; NID:gi180664; PIDN:AAA35699.1; PID:gi180665
A;Note: part of this sequence was confirmed by protein sequencing of the proenzyme
R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harr
Biochem. J. 240, 913-916, 1986
A;Title: Comparison of human stromelysin and collagenase by cloning and sequence anal
A;Reference number: A90336; MUID:87156645
A;Accession: D29157
A;Molecule type: mRNA
A;Residues: 1-199, 'H', 201-207, 'T', 209-469 <MHI>
A;Cross-references: EMBL:X05231; NID:g38266; PIDN:CAA28858.1; PID:g38267
A;Note: parts of this sequence, including the amino end of the proenzyme and of the m
R;Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Show, A.S.; Birkedal-Hansen, H.
Biochemistry 27, 6751-6758, 1988
A;Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzy
end of the activated enzyme.
A;Reference number: A44518; MUID:89062403

A:Accession: A44518
A:Molecule type: protein
A:Residues: 270-305 <BIR>
R:Clark, I.M.; Cawston, T.E.
Biochem. J. 263, 201-206, 1989
A:Title: Fragments of human fibroblast collagenase. Purification and characterization.
A:Reference number: S06132; MUID:90104231
A:Accession: S06132
A:Status: preliminary
A:Molecule type: protein
A:Residues: 100-102, 'P', 104-107, 'XX', 110-112, 270-277, 'X', 279-280, 'X', 282-287 <CLA>
R:Lark, M.W.; Walakovic, L.A.; Shah, T.K.; Vanmiddlesworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A:Title: Production and purification of prostromelysin and procollagenase from IL-1 beta
A:Reference number: A60964; MUID:91059606
A:Accession: B60964
A:Molecule type: protein
A:Residues: 24-35; 100-108; 270-272, 'X', 274, 'X', 276 <LAR>
R:Suzuki, K.; Nagase, H.; Ito, A.; Enghild, J.J.; Salvesen, G.
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990
A:Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rheu
A:Reference number: S10595; MUID:90380300
A:Accession: S10595
A:Molecule type: protein
A:Residues: 20-102 <SUZ>
R:Suzuki, K.; Lees, M.; Newlands, G.F.J.; Nagase, H.; Woolley, D.E.
Biochem. J. 305, 301-306, 1995
A:Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collagen
A:Reference number: S53438; MUID:95126921
A:Accession: S53438
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-108 <SUZ>
R:Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990
A:Title: Multiple modes of activation of latent human fibroblast collagenase: evidence f
A:Reference number: A44517; MUID:90115877
A:Contents: annotation; disulfide bond; activation mechanism
R:Salowe, S.P.; Marcy, A.I.; Cucca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Hermes
Biochemistry 31, 4535-4540, 1992
A:Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry of
A:Reference number: A43031; MUID:92256384
A:Contents: annotation; zinc ligand in proenzyme
A:Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the catal
C:Comment: Procollagenase can be activated without removal of the activation peptide. St
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C:Genetics:
A:Gene: GDB:MMPI; CLG
A:Cross-references: GDB:119783; OMIM:120353
A:Map position: 11q22.2-11q22.3
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C:Superfamily: interstitial collagenase; hemopexin repeat homology: matrix metalloprotei
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status experimental <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status experimental <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:120,143/Binding site: zinc, catalytic (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:269-270/Cleavage site: Pro-Ile (autolytic) #status experimental
F:278-466/Disulfide bonds: #status experimental

Query Match 82.5%; Score 33; DB 1; Length 469;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
||| ||
Db 398 WRYDEY 403

RESULT 13
KCPGI
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C:Accession: S15986; S13597
R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation
A:Reference number: S15986; MUID:91333421
A:Accession: S15986
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-469 <RIC>
A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed
R:Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
Nucleic Acids Res. 18, 6703, 1990
A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PC
A:Reference number: S13597; MUID:91067477
A:Accession: S13597
A:Molecule type: mRNA
A:Residues: 25-469 <CLA>
A:Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269
R:Li, J.; Brick, P.; Blow, D.M.
submitted to the Brookhaven Protein Data Bank, April 1995
A:Reference number: A65568; PDB:1FBL
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
C:Comment: Procollagenase can be activated without removal of the activation peptide.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins,
A:Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
C:Superfamily: interstitial collagenase; hemopexin repeat homology: matrix metallopro
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metal
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status predicted <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #stat
F:120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F:219/Active site: Glu #status predicted
F:278-466/Disulfide bonds: #status experimental

Query Match 82.5%; Score 33; DB 1; Length 469;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
||| ||
Db 398 WRYDEY 403

RESULT 14
KCB01
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C:Accession: S14654; S20336; S14655
R:Tamura, M.; Shimokawa, H.; Sasaki, S.
submitted to the EMBL Data Library, March 1991

Search completed: November 8, 2000, 07:25:57
Job time: 110 sec

A:Reference number: S14654
A:Accession: S14654
A:Molecule type: mRNA
A:Residues: 1-469 <TAM>
A:Cross-references: EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260
R:Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
Arch. Biochem. Biophys. 293, 370-376, 1992
A:Title: Purification and characterization of bovine interstitial collagenase and tissue
A:Reference number: S20336; MUID:92161820
A:Accession: S20336
A:Molecule type: protein
A:Residues: 19-21,'FP',24-29,'L',31-34,'LT',37-39,'F',86-105,'NPR',109-112,'D',114-125 <
C:Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the
C:Comment: procollagenase can be activated without removal of the activation peptide. See
tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-469/Product: procollagenase #status predicted <SIG>
F:19-99/Domain: activation peptide #status predicted <PRO>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:278-466/Disulfide bonds: #status predicted

Query Match 82.5%; Score 33; DB 1; Length 469;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
||| ||
Db 398 WRYDEY 403

RESULT 15
A71707
lipopolysaccharide 1,2-glucosyltransferase (rfaj) RP476 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 08-Oct-1999
C:Accession: A71707
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: A71707
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-517 <AND>
A:Cross-references: GB:AJ235271; GB:AJ235269; NID:g3860788; PIDN:CAAL4931.1; PID:el34277
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: rfaj; RP476

Query Match 82.5%; Score 33; DB 2; Length 517;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryre 5
|||||
Db 505 WRYRE 509

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:25:27 ; Search time 8.6 seconds
(without alignments)
22.289 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	92.5	254	1 MLA_VISAL	P81446 viscum albu
2	37	92.5	400	1 HUTI_PSEPU	O31200 pseudomonas
3	35	87.5	169	1 Y769_METJA	O58179 methanococc
4	33	82.5	334	1 DPOB_RAT	P06766 rattus norv
5	33	82.5	405	1 THRC_METJA	O58860 methanococc
6	33	82.5	468	1 COGI_RABIT	P13943 oryctolagus
7	33	82.5	469	1 COGI_BOVIN	P28053 bos taurus
8	33	82.5	469	1 COGI_HORSE	Q9xs25 equus cabal
9	33	82.5	469	1 COGI_HUMAN	P03956 homo sapien
10	33	82.5	469	1 COGI_PIG	P21692 sus scrofa
11	33	82.5	635	1 STR_SVNV3	P72854 synechocyst
12	33	82.5	641	1 SAC2_YEAST	P39904 saccharomyc
13	33	82.5	831	1 NAPA_ALCEU	P39185 alcaligenes
14	33	82.5	831	1 NAPA_PAPDT	Q56350 paracoccus
15	33	82.5	831	1 NAPA_RHOSH	O53176 rhodobacter
16	32	80.0	315	1 SINR_SALTY	P37459 salmonella
17	32	80.0	2109	1 RRPL_VSVJH	P13615 vesicular s
18	32	80.0	2109	1 RRPL_VSVJO	P16379 vesicular s
19	31	77.5	1230	1 UGS4_SOLTU	Q43846 solanum tub
20	30	75.0	185	1 YGFA_HAEIN	P44528 haemophilus
21	30	75.0	243	1 YQEF_BACSU	P54451 bacillus su
22	30	75.0	307	1 SXL_MEGSC	O01671 megaselia s
23	30	75.0	333	1 DPOB_XENLA	O57383 xenopus lae
24	30	75.0	334	1 DPOB_HUMAN	P06746 homo sapien
25	30	75.0	451	1 Y483_MYCTU	Q11149 mycobacteri
26	30	75.0	466	1 GPT_LEIME	P42864 leishmania
27	30	75.0	610	1 C4BP_BOVIN	Q28065 bos taurus
28	30	75.0	662	1 FTSH_CAPAN	O39444 capsicum an
29	30	75.0	709	1 FTSH_ARATH	Q39102 arabidopsis
30	30	75.0	729	1 FADP_ECOLI	P21177 e fatty oxl
31	30	75.0	749	1 SPOT_SPIC1	Q34098 spiropasma
32	30	75.0	760	1 RELA_CORGL	O87331 corynebacte
33	30	75.0	787	1 RELA_MYCLE	Q49640 mycobacteri

RESULT 1

ID	MLA_VISAL	STANDARD;	PRT;	254 AA.
AC	P81446;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	BETA-GALACTOSIDE SPECIFIC LECTIN I A CHAIN (MLA) (ML-I A) (RRNA N-GLYCOSIDASE) (EC 3.2.2.22).			
OS	Viscum album (European mistletoe).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Santalales; Viscaceae;			
OC	Viscum.			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE: 97134581.			
RA	Huguet Soler M., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T., Voelter W.;			
RT	"Complete amino acid sequence of the A chain of mistletoe lectin I.";			
RL	FEBS Lett. 399:153-157(1996).			
CC	- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).			
CC	- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.			
CC	- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.			
CC	- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA'.			
CC	- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.			
CC	INTERPRO: IPR001574; .			
DR	PFAM: PF00161; RIP; 1.			
DR	PRINTS: PR00396; SHIGARICIN.			
DR	PROSITE: PS00275; SHIGA_RICIN; FALSE_NEG.			
KW	Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.			
FT	ACT_SITE 165 165 BY SIMILARITY.			
FT	CARBOHYD 112 112 N-LINKED (GLCNAC. .).			
FT	VARIANT 15 15 E -> D (IN MLA').			
FT	VARIANT 66 66 V -> I (IN MLA').			
FT	VARIANT 112 112 N -> T (IN MLA').			
FT	VARIANT 116 116 P -> T (IN MLA').			
FT	VARIANT 134 134 DQ -> EE (IN MLA').			
FT	VARIANT 140 140 T -> S (IN MLA').			
FT	VARIANT 144 144 F -> Y (IN MLA').			
FT	VARIANT 151 151 Y -> D (IN MLA').			
FT	VARIANT 179 179 Y -> D (IN MLA').			
FT	VARIANT 184 184 A -> E (IN MLA').			
FT	VARIANT 190 190 V -> M (IN MLA').			
FT	VARIANT 218 218 I -> F (IN MLA').			
FT	VARIANT 223 224 PP -> ST (IN MLA').			
FT	VARIANT 231 231 T -> S (IN MLA').			
FT	VARIANT 235 235 D -> S (IN MLA').			
SQ	SEQUENCE 254 AA; 28478 MW; 53BAF98D3E0FFE67 CRC64;			

Q50638 mycobacteri
P38863 saccharomyc
P52296 rattus norv
P22543 saccharomyc
Q14974 homo sapien
P70168 mus musculu
P27399 simian foam
P20146 notechilis sc
P05748 saccharomyc
P54780 saccharomyc
P20202 sulfolobus
P48874 hansenula w

Query Match 92.5%; Score 37; DB 1; Length 254;
 Best Local Similarity 83.3%; Pred. No. 1.9; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
 ||||:|
 Db 174 WRYRQY 179

RESULT 2

HUTI_PSEPU
 ID HUTI_PSEPU STANDARD; PRT; 400 AA.
 AC O31200;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IMIDAZOLONEPROPIONASE (EC 3.5.2.7) (IMIDAZOLONE-5-PROPIONATE
 DE HYDROLASE).
 GN HUTI.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN=ATCC 12633;
 RA Phillips A.T., Baker C.S.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 4-IMIDAZOLONE-5-PROPIONATE + H(2)O = N-
 CC FORMIMINO-L-GLUTAMATE.
 CC -1- PATHWAY: THIRD STEP IN HISTIDINE DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO THE HUTI FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF032970; AAB86968.1; -;
 DR INTERPRO; IPR002604; -;
 DR PFAM; PF01685; ATZ_TRZ; 1;
 KW Hydrolase; Histidine metabolism.
 SQ SEQUENCE 400 AA; 43146 MW; B47AA19851177991 CRC64;

Query Match 92.5%; Score 37; DB 1; Length 400;
 Best Local Similarity 83.3%; Pred. No. 3.1;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
 ||||:|
 Db 95 WRYRQY 100

RESULT 3

Y769_METJA
 ID Y769_METJA STANDARD; PRT; 169 AA.
 AC Q58179;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ0769.
 GN MJ0769.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE; 96337999.
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -----
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 CC -----
 CC EMBL; U67522; AAB98774.1; -;
 DR TIGR; MJ0769; -;
 KW Hypothetical protein.
 SQ SEQUENCE 169 AA; 20167 MW; C1DEDFB1EF123898 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 169;
 Best Local Similarity 83.3%; Pred. No. 3.1;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
 |||||
 Db 121 WEYREY 126

RESULT 4

DPOB_RAT
 ID DPOB_RAT STANDARD; PRT; 334 AA.
 AC P06766;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DNA POLYMERASE BETA (EC 2.7.7.7).
 GN POLB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE; 87250529.
 RA Matsukage A., Nishikawa K., Ooi T., Seto Y., Yamaguchi M.;
 RA "Homology between mammalian DNA polymerase beta and terminal
 RA deoxynucleotidyltransferase.";
 RL J. Biol. Chem. 262:8960-8962(1987).
 RN [2]
 RC SEQUENCE FROM N.A.
 RX STRAIN=WISTAR;
 RA Konopinski R., Nowak R., Siedlecki J.A.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE OF 17-334 FROM N.A.
 RX MEDLINE; 86259741.
 RA Zmudzka B.Z., Sengupta D., Matsukage A., Cobianchi F., Kumar P.,
 RA Wilson S.H.;
 RT "Structure of rat DNA polymerase beta revealed by partial amino acid
 RT sequencing and cDNA cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5106-5110(1986).
 RN [4]
 RC PARTIAL SEQUENCE, AND REVISION TO 227.
 RX MEDLINE; 90130463.
 RA Kumar P., Widen S.G., Williams K.R., Kedar P., Karpel R.L.,
 RA Wilson S.H.;

RT "Studies of the domain structure of mammalian DNA polymerase beta.
 RT Identification of a discrete template binding domain.";
 RL J. Biol. Chem. 265:2124-2131(1990).
 RN [5]
 RP IMPORTANCE OF ARG-182 IN PRIMER BINDING.
 RX MEDLINE: 9033195.
 RA Date T., Yamamoto S., Tanihara K., Nishimoto Y., Liu N., Matsukage A.;
 RT "Site-directed mutagenesis of recombinant rat DNA polymerase beta:
 RT Involvement of arginine-183 in primer recognition.";
 RL Biochemistry 29:5027-5034(1990).
 RN [6]
 RP IMPORTANCE OF ASP-189 AND ASP-191 IN PRIMER BINDING.
 RX MEDLINE: 91242437.
 RA Date T., Yamamoto S., Tanihara K., Nishimoto Y., Matsukage A.;
 RT "Aspartic acid residues at positions 190 and 192 of rat DNA
 RT polymerase beta are involved in primer binding.";
 RL Biochemistry 30:5286-5292(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE: 94185171.
 RA Davies J.F. II, Almasy R.J., Hostomska Z., Ferre R.A., Hostomsky Z.;
 RT "2.3-A crystal structure of the catalytic domain of DNA polymerase
 RT beta.";
 RL Cell 76:1123-1133(1994).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE: 94278498.
 RA Sawaya M.R., Pelletier H., Kumar A., Wilson S.H., Kraut J.;
 RT "Crystal structure of rat DNA polymerase beta: evidence for a common
 RT polymerase mechanism.";
 RL Science 264:1930-1935(1994).
 RN [9]
 RP STRUCTURE BY NMR OF 1-86.
 RX MEDLINE: 96224818.
 RA Liu D., Prasad R., Wilson S.H., Derose E.F., Mullen G.P.;
 RT "Three-dimensional solution structure of the N-terminal domain of DNA
 RT polymerase beta and mapping of the ssDNA interaction interface.";
 RL Biochemistry 35:6188-6200(1996).
 CC -|- FUNCTION: REPAIR POLYMERASE. CONDUCTS "CAP-FILLING" DNA SYNTHESIS
 CC IN A STEPWISE DISTRIBUTIVE FASHION RATHER THAN IN A PROCESSIVE
 CC FASHION AS FOR OTHER DNA POLYMERASES.
 CC CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
 CC N PYROPHOSPHATE + DNA(N).
 CC -|- SUBUNIT: MONOMER.
 CC -|- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
 CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
 CC DIFFERENT REACTIONS OF DNA SYNTHESIS.
 CC -|- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-X FAMILY.
 CC -----
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 CC -----
 DR EMBL: J02776; AAA41901.1; -;
 DR EMBL: U38801; AAB00389.1; -;
 DR EMBL: M13961; AAA41900.1; -;
 DR PIR: A25445; A25445.
 DR PIR: A27112; A27112.
 DR PIR: A35034; A35034.
 DR PDB: 1BPB; 15-OCT-94.
 DR PDB: 2BPC; 31-AUG-94.
 DR PDB: 1BPD; 15-OCT-94.
 DR PDB: 1BPE; 15-OCT-94.
 DR PDB: 2BPE; 31-AUG-94.
 DR PDB: 2BPG; 31-AUG-94.
 DR PDB: 1RPL; 26-JAN-95.
 DR PDB: 1BNO; 07-DEC-96.
 DR PDB: 1BNP; 07-DEC-96.
 DR PDB: 1NOM; 15-NOV-96.

DR PDB; 1ZQU; 15-NOV-96.
 DR PDB; 1ZQV; 15-NOV-96.
 DR PDB; 1ZQW; 15-NOV-96.
 DR PDB; 1ZQX; 15-NOV-96.
 DR PDB; 1ZQY; 15-NOV-96.
 DR PDB; 1ZQZ; 15-NOV-96.
 DR INTERPRO: IPR002008; -;
 DR INTERPRO: IPR002054; -;
 DR PFAM: PF00966; DNA_polymerase_x; 1.
 DR PRINTS: PR00869; DNAPOLXB.
 DR PRINTS: PR00870; DNAPOLXBETA.
 DR PROSITE: PS00522; DNA_POLYMERASE_X; 1.
 KW Transferrase; DNA-directed DNA polymerase; DNA replication;
 KW 3D-structure.
 FT INIT_MET 0
 FT ACT_SITE 182 182 INVOLVED IN PRIMER BINDING.
 FT ACT_SITE 189 189 INVOLVED IN PRIMER BINDING.
 FT ACT_SITE 191 191 INVOLVED IN PRIMER BINDING.
 FT MUTAGEN 189 189 D->E,S: LOSS OF ACTIVITY.
 FT MUTAGEN 190 190 M->I: NO LOSS OF ACTIVITY.
 FT MUTAGEN 190 190 M->T: 50% LOSS OF ACTIVITY.
 FT MUTAGEN 191 191 D->E,S: LOSS OF ACTIVITY.
 FT CONFLICT 227 227 L -> R (IN REF. 1, 2 AND 3).
 FT TURN 11 11
 FT HELIX 12 27
 FT HELIX 30 30
 FT HELIX 34 49
 FT HELIX 57 62
 FT HELIX 68 79
 FT HELIX 84 91
 FT TURN 93 93
 FT HELIX 94 103
 FT TURN 105 106
 FT HELIX 109 116
 FT TURN 117 119
 FT HELIX 123 126
 FT TURN 127 128
 FT HELIX 130 132
 FT HELIX 135 147
 FT TURN 148 148
 FT HELIX 153 170
 FT TURN 172 173
 FT STRAND 175 178
 FT TURN 181 185
 FT STRAND 192 197
 FT TURN 199 200
 FT TURN 203 204
 FT TURN 209 209
 FT HELIX 210 221
 FT TURN 222 223
 FT STRAND 225 231
 FT STRAND 235 241
 FT STRAND 251 258
 FT TURN 261 263
 FT HELIX 264 272
 FT HELIX 275 287
 FT TURN 288 289
 FT STRAND 290 293
 FT TURN 294 295
 FT STRAND 296 299
 FT TURN 302 303
 FT HELIX 315 321
 FT TURN 322 322
 FT TURN 330 331
 SQ SEQUENCE 334 AA; 38195 MW; 1EDFB8CF0C55FBFA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 334;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryre 5
 |||||

```

Db 324 WYRE 328
RESULT 5
THRC_METJA
ID THRC_METJA STANDARD; PRT; 405 AA.
AC Q5860;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROBABLE THREONINE SYNTHASE (EC 4.2.99.2).
GN THRC OR MJ1465.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY: O-PHOSPHO-L-HOMOSERINE + H(2)O = L-THREONINE
CC + ORTHOPHOSPHATE.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- PATHWAY: THREONINE BIOSYNTHESIS.
CC -----
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CC -----
CC EMBL; U67587; AAB99473.1; -.
CC TIGR; MJ1465; -.
CC INTERPRO; IPR001926; -.
CC PFAM; PF00291; S_T_dehydratase; 1.
CC PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Threonine biosynthesis; Lyase; Pyridoxal phosphate.
FT BINDING 106 106 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 405 AA; 44600 MW; FAD055FB041E2DF0 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 405;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
|||||
Db 53 WRYLEY 58
RESULT 6
COGL_RABIT
ID COGL_RABIT STANDARD; PRT; 468 AA.
AC P13943;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERSTITIAL COLLAGENASE PRECURSOR (EC 3.4.24.7) (MATRIX
DE METALLOPROTEINASE-1) (MMP-1).
GN MMP1.
OS Oryctolagus cuniculus (Rabbit).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SYNOVIAL CELL;
RX MEDLINE; 88077876.
RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
RT "A gene for rabbit synovial cell collagenase: member of a family of
RT metalloproteinases that degrade the connective tissue matrix."
RL Biochemistry 26:6156-6165(1987).
RN [2]
RP SEQUENCE OF 449-468 FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RX MEDLINE; 87029174.
RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
RA Brinckerhoff C.E.;
RT "Homology between exon-containing portions of rabbit genomic clones
RT for synovial cell collagenase and human foreskin and synovial cell
RT mRNAs."
RL Coll. Relat. Res. 6:239-248(1986).
CC -1- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -1- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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CC -----
CC EMBL; M17823; AAB88016.1; -.
CC EMBL; M17820; AAB88016.1; JOINED.
CC EMBL; M17821; AAB88016.1; JOINED.
CC EMBL; M17822; AAB88016.1; JOINED.
CC EMBL; M19240; AAB88016.1; JOINED.
CC EMBL; M25663; AAA31203.1; -.
CC PIR; A27500; KCRBI.
CC HSP; P03956; IGLI.
CC INTERPRO; IPR000130; -.
CC INTERPRO; IPR000585; -.
CC INTERPRO; IPR001818; -.
CC PFAM; PF00413; Peptidase_M10; 1.
CC PFAM; PF00045; hemopexin; 4.
CC PRINTS; PR00138; MATRIXIN
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Signal.
FT SIGNAL 1 18
FT PROPEP 19 98 ACTIVATION PEPTIDE.
FT CHAIN 99 468 INTERSTITIAL COLLAGENASE.
FT DOMAIN 89 96 AUTOINHIBITOR REGION.
FT DOMAIN 274 468 HEMOPEXIN-LIKE.
FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (PROBABLE).
FT METAL 217 217 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 218 218 BY SIMILARITY.
FT METAL 221 221 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 227 227 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 277 465 PROBABLE.
SQ SEQUENCE 468 AA; 53739 MW; DA90538919952B8C CRC64;

Query Match 82.5%; Score 33; DB 1; Length 468;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 wryrey 6
 |||||
 Db 397 WRYDEY 402

Query Match 82.5%; Score 33; DB 1; Length 469;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 7
COGL_BOVIN
ID COGL_BOVIN STANDARD; PRT; 469 AA.
AC P28053;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE INTERSTITIAL COLLAGENASE PRECURSOR (EC 3.4.24.7) (MATRIX
DE METALLOPROTEINASE-1) (MMP-1) (FIBROBLAST COLLAGENASE).
GN MMP1 OR CLG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIODONTIUM FIBROBLAST;
RX MEDLINE; 95201294.
RA Tamura M., Shimokawa H., Sasaki S.;
RT *Primary structure of bovine interstitial collagenase deduced from
RT cDNA sequence.*;
RL DNA Seq. 5:63-66(1994).
CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X.
CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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CC
DR EMBL; X58256; CAA41210.1; -
DR PIR; S14654; KCBOI.
DR HSSP; P03956; 2AYK.
DR INTERPRO; IPR000130; -
DR INTERPRO; IPR000585; -
DR INTERPRO; IPR001818; -
DR PFAM; PF00413; Peptidase_M10; 1.
DR PFAM; PF00045; hemoexin; 4.
DR PRINTS; PR00138; MATRXIN.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hyalolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Signal.
FT SIGNAL 1 18
FT PROPEP 19 99
FT CHAIN 100 469
FT DOMAIN 90 97
FT DOMAIN 275 469
FT CARBOHYD 120 120
FT METAL 218 218
FT ACT_SITE 219 219
FT METAL 222 222
FT METAL 228 228
FT DISULFID 278 466
SQ SEQUENCE 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;

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QY 1 wryrey 6
 |||||
 Db 398 WRYDEY 403

Query Match 82.5%; Score 33; DB 1; Length 469;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 8
COGL_HORSE
ID COGL_HORSE STANDARD; PRT; 469 AA.
AC Q9X5Z5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERSTITIAL COLLAGENASE PRECURSOR (EC 3.4.24.7) (MATRIX
DE METALLOPROTEINASE-1) (MMP-1).
GN MMP1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson D.W.;
RT "Cloning and expression of equine matrix metalloproteinase 1
RT (interstitial collagenase).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X.
CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
CC
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CC
DR EMBL; AF148882; AAD38030.1; -
DR INTERPRO; IPR000130; -
DR INTERPRO; IPR000585; -
DR INTERPRO; IPR001818; -
DR PFAM; PF00413; Peptidase_M10; 1.
DR PFAM; PF00045; hemoexin; 4.
DR PRINTS; PR00138; MATRXIN.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hyalolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Signal.
FT SIGNAL 1 18
FT PROPEP 19 99
FT CHAIN 100 469
FT DOMAIN 90 97
FT DOMAIN 275 469
FT CARBOHYD 120 120
FT METAL 218 218
FT ACT_SITE 219 219
FT METAL 222 222
FT METAL 228 228
FT DISULFID 278 466
SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;

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Query Match 82.5%; Score 33; DB 1; Length 469;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CC  EMBL; X05231; CAA28858.1; -
CC  EMBL; M13509; AAA35699.1; -
DR  EMBL; M16567; AAA52033.1; -
DR  EMBL; U78045; AAB36941.1; -
DR  EMBL; M15996; AAA35700.1; -
DR  EMBL; X54925; CAA38691.1; -
DR  PIR; A37308; KCHUI.
DR  PDB; 1CGE; 31-MAR-95.
DR  PDB; 1CGF; 31-MAR-95.
DR  PDB; 1CGL; 27-FEB-95.
DR  PDB; 1HFC; 26-JAN-95.
DR  PDB; 2TCL; 08-MAR-96.
DR  PDB; 1AYK; 25-FEB-98.
DR  PDB; 2AYK; 25-FEB-98.
DR  MIM; 120353; -.
DR  INTERPRO; IPR000130; -.
DR  INTERPRO; IPR000585; -.
DR  INTERPRO; IPR001818; -.
DR  PFAM; PF00413; Peptidase_M10; 1.
DR  PFAM; PF00045; hemopexin; 4.
DR  PRINTS; PR00138; MATRINX.
DR  PROSITE; PS00024; HEMOPEXIN; 1.
DR  PROSITE; PS00142; ZINC_PROTEASE; 1.
DR  PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW  Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW  Collagen degradation; Extracellular matrix; Signal; 3D-structure.
FT  SIGNAL 1 19
FT  PROPEP 20 99
FT  CHAIN 100 469
FT  CHAIN 100 269
FT  CHAIN 271 469
FT  DOMAIN 90 97
FT  DOMAIN 98 276
FT  DOMAIN 275 469
FT  CARBOHYD 120 120
FT  METAL 218 218
FT  ACT_SITE 219 219
FT  METAL 222 222
FT  METAL 228 228
FT  DISULFID 278 466
FT  SITE 269 270
FT  CONFLICT 43 43
FT  CONFLICT 64 64
FT  CONFLICT 115 115
FT  CONFLICT 200 200
FT  CONFLICT 208 208
FT  CONFLICT 317 317
FT  CONFLICT 410 410
SQ  SEQUENCE 469 AA; 54007 MW; 4B1361DCF4C54B20 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 469;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
Db 398 WRYDEY 403

RESULT 10
COGI_PIG
ID COGI_PIG STANDARD; PRT; 469 AA.
AC P21692;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERSTITIAL COLLAGENASE PRECURSOR (EC 3.4.24.7) (MATRIX
DE METALLOPROTEINASE-1) (MMP-1).

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GN MMPI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 91333421.
RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
RL modulation of expression of RNA in vitro by various cytokines.";
RN [2]
RP SEQUENCE OF 25-469 FROM N.A.
RX TISSUE-SYNOVIAL CELL;
RC MEDLINE; 91067477.
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
RL obtained by PCR.";
RN [3]
RP Nucleic Acids Res. 18:6703-6703(1990).
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
RX Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
RT "Structure of full-length porcine synovial collagenase reveals a C-
RL terminal domain containing a calcium-linked, four-bladed
beta-propeller.";
RN [4]
RP Structure 3:541-549(1995).
RX SEQUENCE OF 100-104 AND 248-282, AND AUTOLYTIC CLEAVAGE SITE.
RA MEDLINE; 95142615.
RX Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
RA O'Hare M.C.;
RT "Recombinant porcine collagenase: purification and autolysis.";
RL Arch. Biochem. Biophys. 316:123-127(1995).
CC -|- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X.
CC -|- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -|- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -|- PTM: UNDERGOES AUTOLYTIC CLEAVAGE TO PRODUCE A N-TERMINAL
CC FRAGMENT HAVING REDUCED COLLAGENOLYTIC ACTIVITY.
CC -|- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIN SUBFAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54724; CAA38526.1; -.
DR PIR; S15986; KCPGI.
DR PDB; 1FBL; 29-JAN-96.
DR INTERPRO; IPR000130; -.
DR INTERPRO; IPR000585; -.
DR INTERPRO; IPR001818; -.
DR PFAM; PF00413; Peptidase_M10; 1.
DR PFAM; PF00045; hemopexin; 4.
DR PRINTS; PR00138; MATRINX.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Signal; 3D-structure.
FT SIGNAL 1 19
FT PROPEP 20 99
FT CHAIN 100 469
FT CHAIN 100 258

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FT DOMAIN 90 97 AUTOINHIBITOR REGION.
FT FT 275 469 HEMOPLEXIN-LIKE (BY SIMILARITY).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT METAL 218 218 ZINC (CATALYTIC).
FT ACT_SITE 219 219
FT METAL 222 222 ZINC (CATALYTIC).
FT METAL 228 228 ZINC (CATALYTIC).
FT METAL 278 278 PROBABLE.
FT SITE 258 259 CLEAVAGE (AUTOLYTIC).
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 469;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 wryrey 6
   ||| ||
Db 398 WRYDEY 403

RESULT 11
SIR_SYNY3
ID SIR_SYNY3 STANDARD; PRT; 635 AA.
AC P72854;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SULFITE REDUCTASE (FERREDOXIN) (EC 1.8.7.1).
GN SIR OR SLR0963.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpou S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Tasuda M., Tabata S.;
RP "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: H(2)S + 3 OXIDIZED FERREDOXIN + 3 H(2)O =
CC SULFITE + 3 REDUCED FERREDOXIN.
CC -1- COFACTOR: THIS ENZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
CC FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
CC SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
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-----
EMBL; D90901; BAA16869.1; -.
DR HSSP; P17846; 7GEP.
DR INTERPRO; IPR000660; -.
DR PFAM; PF01077; NIR_SIR; 1.
DR PRINTS; PR00397; SIROHAEM.
DR PROSITE; PS00365; NIR_SIR; 1.
KW Oxidoreductase; Heme; Iron-sulfur; 4Fe-4S.
FT METAL 451 451 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 457 457 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 496 496 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 500 500 IRON-SULFUR (4FE-4S) AND SIROHEME
(BY SIMILARITY).
```

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SQ SEQUENCE 635 AA; 71441 MW; 91F4A1B139AD7B34 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 635;
Best Local Similarity 86.7%; Pred. No. 30;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
   |||::|
Db 354 WRYQDY 359

RESULT 12
SAC2_YEAST
ID SAC2_YEAST STANDARD; PRT; 641 AA.
AC P39904; Q03379;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SAC2 PROTEIN.
GN SAC2 OR YDR484W OR D8035.27.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE; 95274323.
RA Koelling R., Lee A., Chen E.Y., Botstein D.;
RT "Nucleotide sequence of the SAC2 gene of Saccharomyces cerevisiae.";
RL Yeast 10:1211-1216(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z29988; CAA82878.1; -.
DR EMBL; U33050; AAB64912.1; -.
DR PIR; S42036; S42036.
DR PIR; S46602; S46602.
DR SGD; S0002892; SAC2.
KW Cytokeleton.
FT CONFLICT 204 209 KRLIIS -> EKYTYF (IN REF. 1).
SQ SEQUENCE 641 AA; 74332 MW; F2BF669A72A712C1 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 641;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 wryrey 6
   | ||||
Db 260 WYREY 265

RESULT 13
NAPA_ALCEU
ID NAPA_ALCEU STANDARD; PRT; 831 AA.
AC P39185;
DT 01-FEB-1995 (Rel. 31, Created)
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DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PERIPLASMIC NITRATE REDUCTASE PRECURSOR (EC 1.7.99.4).
 GN NAPA.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.
 RC STRAIN-H16;
 RX MEDLINE: 93388517.
 RA Siddiqui R.A., Warnecke-Eberz U., Hengsberger A., Schneider B.,
 RA Koscka S., Friedrich B.;
 RT "Structure and function of a periplasmic nitrate reductase in
 RT Alcaligenes eutrophus H16.";
 RL J. Bacteriol. 175:5867-5876(1993).
 CC -!- FUNCTION: LARGE SUBUNIT OF THE PERIPLASMIC NITRATE REDUCTASE
 CC (NAP). ONLY EXPRESSED AT HIGH LEVELS DURING AEROBIC GROWTH. NAPAB
 CC COMPLEX RECEIVES ELECTRONS FROM THE MEMBRANE-ANCHORED TETRAHEME
 CC NACP PROTEIN, THUS ALLOWING ELECTRON FLOW BETWEEN MEMBRANE AND
 CC PERIPLASM. ESSENTIAL FUNCTION FOR NITRATE ASSIMILATION AND MAY
 CC HAVE A ROLE IN ANAEROBIC METABOLISM.
 CC -!- CATALYTIC ACTIVITY: NITRITE + ACCEPTOR = NITRATE + REDUCED
 CC ACCEPTOR.
 CC -!- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN); MAY BIND A 4FE-4S CLUSTER.
 CC -!- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A CYTOCHROME C.
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -!- INDUCTION: EXPRESSED INDEPENDENTLY OF NITRATE INDUCTION AND
 CC ANAEROBIOSIS.
 CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY. NASA/NAPA/NARB SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X71385; CAA50507.1; -.
 DR PIR; A48489; A48489.
 DR INTERPRO; IPR001467; -.
 DR PFAM; PF01568; Molybdop_binding; 1.
 DR PFAM; PF00384; molybdoppterin; 1.
 DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
 DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; FALSE_NEG.
 DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; FALSE_NEG.
 KW Nitrate assimilation; Oxidoreductase; Electron transport; Molybdenum;
 KW Periplasmic; Signal; Iron-sulfur; 4Fe-4S.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 831 PERIPLASMIC NITRATE REDUCTASE.
 FT METAL 48 48 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 51 51 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 55 55 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 83 83 IRON-SULFUR (4FE-4S) (POTENTIAL).
 SQ SEQUENCE 831 AA; 93309 MW; B033D5A70ECF4B38 CRC64;
 Query Match 82.5%; Score 33; DB 1; Length 831;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wzyre 5
 DB 671 WYRE 675
 RESULT 14
 ID NAPA_PARDT STANDARD; PRT; 831 AA.
 AC Q56350;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PERIPLASMIC NITRATE REDUCTASE PRECURSOR (EC 1.7.99.4).
 GN NAPA.
 OS Paracoccus denitrificans (subsp. thiosphaera pantotropha).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Paracoccus.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-ATCC 35512 / LMD 82.5;
 RX MEDLINE: 95368980.
 RA Berks B.C., Richardson D.J., Reilly A., Willis A.C., Ferguson S.J.;
 RA "The napEDABC gene cluster encoding the periplasmic nitrate reductase
 RT system of Thiosphaera pantotropha.";
 RL Biochem. J. 309:983-992(1995).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN-M-6;
 RX MEDLINE: 94164150.
 RA Berks B.C., Richardson D.J., Robinson C., Reilly A., Applin R.T.,
 RA Ferguson S.J.;
 RT "Purification and characterization of the periplasmic nitrate
 RT reductase from Thiosphaera pantotropha.";
 RL Eur. J. Biochem. 220:117-124(1994).
 RN [3]
 RP CHARACTERIZATION, AND SEQUENCE OF 642-655 AND 699-715.
 RC STRAIN-M-6;
 RX MEDLINE: 94252409.
 RA Breton J., Berks B.C., Reilly A., Thomson A.J., Ferguson S.J.,
 RA Richardson D.J.;
 RT "Characterization of the paramagnetic iron-containing redox centres
 RT of Thiosphaera pantotropha periplasmic nitrate reductase.";
 RL FEBS Lett. 345:76-80(1994).
 CC -!- FUNCTION: LARGE SUBUNIT OF THE PERIPLASMIC NITRATE REDUCTASE
 CC (NAP). ONLY EXPRESSED AT HIGH LEVELS DURING AEROBIC GROWTH. NAPAB
 CC COMPLEX RECEIVES ELECTRONS FROM THE MEMBRANE-ANCHORED TETRAHEME
 CC NACP PROTEIN, THUS ALLOWING ELECTRON FLOW BETWEEN MEMBRANE AND
 CC PERIPLASM. ESSENTIAL FUNCTION FOR NITRATE ASSIMILATION AND MAY
 CC HAVE A ROLE IN ANAEROBIC METABOLISM.
 CC -!- CATALYTIC ACTIVITY: NITRITE + ACCEPTOR = NITRATE + REDUCED
 CC ACCEPTOR.
 CC -!- COFACTOR: BINDS THE GMP DERIVATIVE OF THE MOLYBDOPTERIN (MGD). MAY
 CC BIND A 4FE-4S CLUSTER.
 CC -!- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A CYTOCHROME C.
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY. NASA/NAPA/NARB SUBFAMILY.
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 CC -----
 CC EMBL: Z36773; CAA85346.1; -.
 DR INTERPRO; IPR001467; -.
 DR PFAM; PF01568; Molybdop_binding; 1.
 DR PFAM; PF00384; molybdoppterin; 1.
 DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
 DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; FALSE_NEG.
 DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; FALSE_NEG.
 KW Nitrate assimilation; Oxidoreductase; Electron transport; Molybdenum;
 KW Periplasmic; Signal; Iron-sulfur; 4Fe-4S.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 831 PERIPLASMIC NITRATE REDUCTASE.
 FT METAL 48 48 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 51 51 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 55 55 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 83 83 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 128 128 T -> D (IN AA SEQUENCE).
 SQ SEQUENCE 831 AA; 92617 MW; ED78963BD2DA2144 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 831;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wryre 5
Db 671 WRYRE 675

FT METAL 83 83 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 831 AA; 92806 MW; EDEB18AFPC52ESC CRC64;

Query Match 82.5%; Score 33; DB 1; Length 831;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wryre 5
Db 671 WRYRE 675

Search completed: November 8, 2000, 07:27:11
Job time: 104 sec

Query Match 82.5%; Score 33; DB 1; Length 831;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wryre 5
Db 671 WRYRE 675

RESULT 15
NAPA_RHOSH
ID NAPA_RHOSH STANDARD; PRT; 831 AA.
AC Q53176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PERIPLASMIC NITRATE REDUCTASE PRECURSOR (EC 1.7.99.4).
GN NAPA.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE: 96332666.
RA Reyes F., Roldan M.D., Klipp W., Castillo F., Moreno-Vivian C.;
RT "Isolation of periplasmic nitrate reductase genes from Rhodobacter
sphaeroides DSM 158: structural and functional differences among
prokaryotic nitrate reductases";
RL Mol. Microbiol. 19:1307-1318(1996).
CC -1- FUNCTION: LARGE SUBUNIT OF THE PERIPLASMIC NITRATE REDUCTASE
(NAP). ONLY EXPRESSED AT HIGH LEVELS DURING AEROBIC GROWTH. NAPAB
COMPLEX RECEIVES ELECTRONS FROM THE MEMBRANE-ANCHORED TETRAHEME
NAPC PROTEIN, THUS ALLOWING ELECTRON FLOW BETWEEN MEMBRANE AND
PERIPLASM. ESSENTIAL FUNCTION FOR NITRATE ASSIMILATION AND MAY
HAVE A ROLE IN ANAEROBIC METABOLISM.
CC -1- CATALYTIC ACTIVITY: NITRITE + ACCEPTOR = NITRATE + REDUCED
ACCEPTOR.
CC -1- COFACTOR: BINDS THE GMP DERIVATIVE OF THE MOLYBDOPTERIN (MGD). MAY
BIND A 4FE-4S CLUSTER (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A CYTOCHROME C (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- INDUCTION: NITRATE REDUCTASE ACTIVITY CAN BE INDUCED BY NITRATE
AND NOT REPRESSED BY AMMONIUM OR OXYGEN.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
OXIDOREDUCTASE FAMILY. NAPA/NARB SUBFAMILY.

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DR EMBL: Z46806; CAA86827.1; -.
DR INTERPRO: IPR001467; -.
DR PFAM: PF01568; Molybdop_binding; 1.
DR PFAM: PF00384; molybdopterin; 1.
DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; 1.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; FALSE_NEG.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; FALSE_NEG.
KW Nitrate assimilation; Oxidoreductase; Electron transport; Molybdenum;
KW Periplasmic; Signal; Iron-sulfur; 4Fe-4S.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 831 PERIPLASMIC NITRATE REDUCTASE.
FT DOMAIN 11 21 POLY-ALA.
FT METAL 48 48 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 51 51 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 55 55 IRON-SULFUR (4FE-4S) (POTENTIAL).

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:25:13 ; Search time 17.9 Seconds
(without alignments)
31.299 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL14:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phase:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	404	1 029700	029700 archaeoglob
2	36	90.0	406	1 026354	026354 methanobact
3	36	90.0	642	2 066684	066684 aquifex aeo
4	35	87.5	329	2 083509	083509 treponema p
5	33	82.5	175	6 097773	097773 sus scrofa
6	33	82.5	192	12 077374	077374 human immun
7	33	82.5	192	12 079667	079667 human immun
8	33	82.5	192	12 091143	091143 human immun
9	33	82.5	250	2 098719	098719 deinococcus
10	33	82.5	276	2 072880	072880 synecocyst
11	33	82.5	402	12 097733	097733 fowl adenov
12	33	82.5	517	2 092D68	092D68 rickettsia
13	33	82.5	653	2 09REB6	09REB6 enterobacte
14	33	82.5	831	2 088111	088111 rhodobacter
15	33	82.5	834	2 0923W4	0923W4 pseudomonas
16	33	82.5	853	2 09RC05	09RC05 pseudomonas
17	33	82.5	986	2 050357	050357 mycoplasma
18	33	82.5	986	2 030380	030380 mycoplasma
19	33	82.5	997	3 012142	012142 saccharomyc

20	33	82.5	1816	5 09W0E3	09W0E3 drosophila
21	33	82.5	4881	2 09S0R3	09S0R3 streptomyce
22	32	80.0	55	2 09XDS5	09XDS5 salmonella
23	32	80.0	229	5 022615	022615 caenorhabdi
24	32	80.0	337	2 050949	050949 neisseria g
25	32	80.0	661	5 018598	018598 caenorhabdi
26	32	80.0	665	5 018597	018597 caenorhabdi
27	32	80.0	783	12 098210	098210 molluscum c
28	31	77.5	174	2 066725	066725 aquifex aeo
29	31	77.5	367	10 09XEG0	09XEG0 arabidopsis
30	31	77.5	390	10 09SFF8	09SFF8 arabidopsis
31	31	77.5	419	2 09X4C7	09X4C7 escherichia
32	31	77.5	438	5 09V3I9	09V3I9 drosophila
33	31	77.5	443	1 09UZ55	09UZ55 pyrococcus
34	31	77.5	454	2 067843	067843 aquifex aeo
35	31	77.5	489	10 09SMG6	09SMG6 dorotheanth
36	31	77.5	567	3 094381	094381 schizosacch
37	31	77.5	594	5 016312	016312 caenorhabdi
38	31	77.5	649	5 044752	044752 caenorhabdi
39	31	77.5	729	10 024397	024397 triticum ae
40	30	75.0	70	2 099343	099343 escherichia
41	30	75.0	74	2 083756	083756 treponema p
42	30	75.0	118	13 042311	042311 coturnixa co
43	30	75.0	166	2 096928	096928 mycobacteri
44	30	75.0	205	13 079774	079774 gallus gall
45	30	75.0	208	13 09PT39	09PT39 oncorhynch

ALIGNMENTS

RESULT 1
029700 PRELIMINARY; PRT; 404 AA.
ID 029700
AC 029700;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE THREONINE SYNTHASE (THRC-1).
GN AF0551.

OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
ON Archaeoglobus.

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343.
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AF001066; AAB90683.1;
DR TIGR; AF0551;
DR INTERPRO; IPR001926;
DR PFAM; PF00291; S_T_dehydratase; 1.
KW Hypothetical protein.

SQ SEQUENCE 404 AA; 43941 MW; 05C2E7770C26050 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 wryrey 6
Db 56 WRYREF 61

RESULT 2
ID O26354 PRELIMINARY; PRT; 406 AA.
AC O26354;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE THEONINE SYNTHASE.
GN MTH253.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE: 98037514.
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., DuBois J.,
RA Aldredge T., Bashirzaden R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RA "Complete genome sequence of Methanobacterium thermoautotrophicum
RT delah: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000812; AAB84759.1; -.
DR INTERPRO: IPR000634; -.
DR INTERPRO: IPR001926; -.
DR PFAM: PF00231; S-T-dehydratase; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
SQ SEQUENCE 406 AA; 43716 MW; 1EB6C981C76B63FA CRC64;

Query Match 90.08; Score 36; DB 1; Length 406;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 53 WRYREF 58

RESULT 3
ID O66684 PRELIMINARY; PRT; 642 AA.
AC O66684;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ATP-DEPENDENT HELICASE (DING FAMILY).
GN DING.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE: 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL: AE000685; AAC06640.1; -.
DR INTERPRO: IPR001410; -.
DR PFAM: PF00270; DEAD; 1.
KW Helicase.

SQ SEQUENCE 642 AA; 75417 MW; 52E1976BE877B936 CRC64;

Query Match 90.08; Score 36; DB 2; Length 642;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 611 WRYREF 616

RESULT 4
ID O83509 PRELIMINARY; PRT; 329 AA.
AC O83509;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN TP0496.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE: 98332770.
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiaich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete.";
RL Science 281:375-388(1998).
DR EMBL: AF001226; AAC65483.1; -.
DR TIGR: TP0496; -.
DR INTERPRO: IPR001440; -.
SQ SEQUENCE 329 AA; 37761 MW; 565B880F279D2589 CRC64;

Query Match 87.5%; Score 35; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
Db 57 WRYREF 62

RESULT 5
ID Q9TT73 PRELIMINARY; PRT; 175 AA.
AC Q9TT73;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MATRIX METALLOPROTEINASE 1 (FRAGMENT).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
RT "Cloning of porcine matrix metalloproteinase 1 (MMP1) partial cDNA.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF202971; AAF23968.1; -.
DR INTERPRO: IPR000585; -.
DR PFAM: PF00045; hemopexin; 3.
DR PROSITE: PS00024; HEMOPEXIN; 1.
FT NON_TER 1 1

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FT NON_TER 175 175
SQ SEQUENCE 175 AA; 20463 MW; C1FDF6D459230181 CRC64;

Query Match 82.5%; Score 33; DB 6; Length 175;
Best Local Similarity 83.3%; Pred. NO. 53;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryrey 6
|||:|

Db 136 WRYDEY 141

RESULT 6 ---

Q77374
ID Q77374 PRELIMINARY; PRT; 192 AA.
AC Q77374
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE VIF PROTEIN.
GN VIF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94149849.
RA Vanden Haesevelde M., DeCourt J.L., De Leys R.J., Vanderborght B.,
der Groen G., Van Heuverswijn H., Saman E.;
RT "Genomic cloning and complete sequence analysis of a highly divergent
RT African human immunodeficiency virus isolate.";
RL J. Virol. 68:1586-1596(1994).
DR EMBL: L20587; AAA99880.1; -.
DR INTERPRO: IPR000475; -.
DR PFAM: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFECT.
DR PRODOM: PD000063; -; 1.
SQ SEQUENCE 192 AA; 22742 MW; F236C302F11A3B48 CRC64;

Query Match 82.5%; Score 33; DB 12; Length 192;
Best Local Similarity 66.7%; Pred. NO. 58;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6

|||:|

Db 89 WRYKKY 94

RESULT 7

Q79667
ID Q79667 PRELIMINARY; PRT; 192 AA.
AC Q79667
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE VIF PROTEIN.
GN VIF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94149848.
RA Gurtler L.G., Hauser P.H., Eberle J., Von Brunn A., Knapp S.,
Zekeng L., Tsague J.M., Kaptue L.;
RT "A new subtype of human immunodeficiency virus type 1 (MVP-5180) from
RT Cameroon.";
RL J. Virol. 68:1581-1585(1994).
DR EMBL: L20571; AAA44861.1; -.
DR INTERPRO: IPR000475; -.
DR PFAM: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFECT.
DR PRODOM: PD000063; -; 1.

SQ SEQUENCE 192 AA; 22657 MW; D5A552D77C90F32E CRC64;

Query Match 82.5%; Score 33; DB 12; Length 192;
Best Local Similarity 66.7%; Pred. NO. 58;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6

|||:|

Db 89 WQYKEY 94

RESULT 8

O91143
ID O91143 PRELIMINARY; PRT; 192 AA.
AC O91143
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE VIF PROTEIN.
GN VIF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCF02;
RA Bibollet-Ruche F., Lousert-Ajaka I., Simon F., Mboup S., Mpoudi N.E.,
Saman E., Delaporte E., Peeters M.;
RT "Genetic characterization of accessory genes from human
RT immunodeficiency viruses type 1 group O.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y16021; CAA75945.1; -.
DR INTERPRO: IPR000475; -.
DR PFAM: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFECT.
DR PRODOM: PD000063; -; 1.
SQ SEQUENCE 192 AA; 22792 MW; 36975A593F7A2EDB CRC64;

Query Match 82.5%; Score 33; DB 12; Length 192;
Best Local Similarity 66.7%; Pred. NO. 58;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryrey 6

|||:|

Db 89 WQYKEY 94

RESULT 9

O9RTJ9
ID O9RTJ9 PRELIMINARY; PRT; 250 AA.
AC O9RTJ9
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HYPOTHETICAL 27.0 KDA PROTEIN.
GN DR1763.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1.
RX MEDLINE: 20036896.
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
RT "Genome Sequence of the Radioresistant Bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).

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DR EMBL; AE002018; AAF11325.1; -.
DR TIGR; DRI763; -.
KW Hypothetical protein.
SQ SEQUENCE 250 AA; 26957 MW; 4C762EA5562200AC CRC64;

Query Match      82.5%; Score 33; DB 2; Length 250;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 6
   ||:|:|
Db 196 WRFERDY 201

RESULT 10
P72880
ID P72880 PRELIMINARY; PRT; 276 AA.
AC P72880;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE ABC TRANSPORTER.
GN SLR0977.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90901; BAA16896.1; -.
DR INTERPRO; IPR000412; -.
DR PFAM; PF01061; ABC3_membrane; 1.
SQ SEQUENCE 276 AA; 31542 MW; 24015C82E02DB371 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 5
   |||||
Db 24 WRYRE 28

RESULT 11
Q9YVR3
ID Q9YVR3 PRELIMINARY; PRT; 402 AA.
AC Q9YVR3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PIV2A HOMOLOG.
OS fowl adenovirus 8.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC A-2A;
RX MEDLINE; 98451338.
RA Cao J.X., Krell P.J., Nagy E.;
RT "Sequence and transcriptional analysis of terminal regions of the
RT fowl adenovirus type 8 genome.";
RL J. Gen. Virol. 79:2507-2516(1998).
[2]
RN SEQUENCE FROM N.A.

RA Ojkic D., Nagy E.;
RT "The DNA sequence of fowl adenovirus 8 ";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF021253; AAC71664.1; -.
DR EMBL; AF083975; AAD50335.1; -.
SQ SEQUENCE 402 AA; 45798 MW; 343965870E5BB19F CRC64;

Query Match      82.5%; Score 33; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 5
   |||||
Db 17 WRYRE 21

RESULT 12
Q9ZD68
ID Q9ZD68 PRELIMINARY; PRT; 517 AA.
AC Q9ZD68;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE LIPOPOLYSACCHARIDE 1,2-GLUCOSYLTRANSFERASE (RFAJ).
GN RP476.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=MADRID E.
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
DR EMBL; AJ235271; CAAL4931.1; -.
DR INTERPRO; IPR002495; -.
DR PFAM; PF01501; Glyco_transf_8; 1.
SQ SEQUENCE 517 AA; 60778 MW; A5C7605371BAFC95 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryrey 5
   |||||
Db 505 WRYRE 509

RESULT 13
Q9REB6
ID Q9REB6 PRELIMINARY; PRT; 653 AA.
AC Q9REB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE MOBB PROTEIN.
GN MOBB.
OS Enterobacter cloacae.
OG Plasmid Clodf13.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
[1]
RN SEQUENCE FROM N.A.
RA Nunez B., Avila P., de la Cruz F.;
RT "Mobilization functions of Clodf13.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ224861; CAB62409.1; -.

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KW Plasmid.
SQ SEQUENCE 653 AA; 72897 MW; D69F5922FE8A79F CRC64;

Query Match 82.5%; Score 33; DB 2; Length 653;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryre 6
| | | | |
Db 26 WLYREY 31

RESULT 14

O88111 PRELIMINARY; PRT; 831 AA.

AC O88111
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PERIPLASMIC NITRATE REDUCTASE PRECURSOR (EC 1.7.99.4).
GN NAPA.

OS Rhodobacter sphaeroides f. sp. denitrificans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.

[1]

RN SEQUENCE FROM N.A.

RC STRAIN-IL 106;
RA Sabaty M., Schwintner C., Cahors C., Richaud P., Vermeglio A.;
RT "The periplasmic nitrate reductase of Rhodobacter sphaeroides f. sp.
RT denitrificans is essential for denitrification."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

[2]

RN SEQUENCE FROM N.A.

RC STRAIN-IL106;
RA Yamamoto I.;
RT "Cloning of the napKEDABC genes encoding a periplasmic nitrate
RT reductase from a denitrifying phototrophic bacterium Rhodobacter
RT sphaeroides f. sp. denitrificans."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF069545; AAC23522.1; -.
DR EMBL; AB016290; BAA31961.1; -.
DR INTERPRO; IPR001467; -.
DR PFAM; PF00384; molybdopterin; 1.
DR PFAM; PF01568; Molybdop_binding; 1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
KW Signal; Oxidoreductase.
FT SIGNAL 1 12 POTENTIAL.
FT CHAIN 13 831 PERIPLASMIC NITRATE REDUCTASE.
SQ SEQUENCE 831 AA; 92710 MW; 2794306F94ABFBF9 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 831;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryre 5
| | | | |
Db 671 WRYRE 675

RESULT 15

Q923W4 PRELIMINARY; PRT; 834 AA.

AC Q923W4
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PERIPLASMIC NITRATE REDUCTASE LARGE SUBUNIT PRECURSOR.
GN NAPA.

OS Pseudomonas sp. G-179.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae.

RN SEQUENCE FROM N.A.
RP STRAIN-G-179;
RC Ye R.W., Bedzyk L., Wang T.;
RA "Identification and Characterization of a DNA Region Involved in
RT Reduction of Nitrate, Nitrite, and Nitric Oxide by the Denitrifying
RT Bacteria Pseudomonas sp. G-179."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083948; AAC79443.1; -.
DR INTERPRO; IPR001467; -.
DR PFAM; PF00384; molybdopterin; 1.
DR PFAM; PF01568; Molybdop_binding; 1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
SQ SEQUENCE 834 AA; 93491 MW; 71B319DD30D46C8E CRC64;

Query Match 82.5%; Score 33; DB 2; Length 834;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryre 5
| | | | |
Db 673 WRYRE 677

Search completed: November 8, 2000, 07:26:59
Job time: 106 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:26:38 ; Search time 13.2 Seconds
(without alignments)
28.846 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues
Total number of hits satisfying chosen parameters: 316

Minimum DB Seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	42.5	6	2 I37027	protamine p1 - gor
2	12	30.0	3	2 A22565	R-phycoerythrin al
3	12	30.0	4	2 I84439	protamine p1 - sav
4	12	30.0	4	2 I61883	protamine p1 - Ora
5	12	30.0	4	2 I37013	protamine p1 - Cer
6	12	30.0	5	1 HOROHA	proctolin - Americ
7	12	30.0	5	2 B37325	pap fibrial regul
8	12	30.0	5	2 I39864	ribosomal protein
9	12	30.0	5	2 I39866	ribosomal protein
10	12	30.0	5	2 I39965	ribosomal protein
11	12	30.0	5	2 F22565	R-phycoerythrin ga
12	12	30.0	5	2 A60411	proctolin - Atlant
13	12	30.0	6	2 A41946	T-cell receptor ga
14	11	27.5	3	2 F37196	bradykinin-potentl
15	11	27.5	4	2 A34626	RPCH-related neuro
16	11	27.5	4	2 B53284	T-cell receptor be
17	11	27.5	4	2 PT0661	T-cell receptor be
18	11	27.5	5	2 A60803	neuropeptide - sea
19	11	27.5	5	2 A44692	fulicin - giant Af
20	11	27.5	5	2 JH0253	gut pentapeptide -
21	11	27.5	5	2 G37196	bradykinin-potentl
22	11	27.5	5	2 PT0281	Ig heavy chain CRD
23	11	27.5	5	2 PT0308	Ig heavy chain CRD
24	11	27.5	5	2 A32516	cholecystokinin-5
25	11	27.5	5	2 PT0729	T-cell receptor be
26	11	27.5	5	2 PT0580	T-cell receptor be
27	11	27.5	6	2 S66195	alcohol dehydrogen
28	11	27.5	6	2 PD0028	pev-kinin 2 - pena
29	11	27.5	6	2 B34835	dnaA protein - Pse

30	11	27.5	6	2 S11556	hydrogensulfite re
31	11	27.5	6	2 B44510	hypothetical prote
32	11	27.5	6	2 A31263	dihydrofolate redu
33	11	27.5	6	2 B31263	dihydrofolate redu
34	11	27.5	6	2 A61068	locustakinin - mig
35	11	27.5	6	2 B35640	cerebellar degener
36	11	27.5	6	2 PT0629	T-cell receptor be
37	11	27.5	6	2 PT0532	T-cell receptor be
38	11	27.5	6	2 PT0519	T-cell receptor be
39	11	27.5	6	2 PT0637	T-cell receptor be
40	11	27.5	6	2 PT0641	T-cell receptor be
41	11	27.5	6	2 PT0726	T-cell receptor be
42	11	27.5	6	2 F41946	T-cell receptor ga
43	11	27.5	6	4 I79564	hypothetical TCL3
44	10	25.0	5	2 T14910	hypothetical prote
45	10	25.0	6	2 B26206	alpha-1,4-glucan-p

ALIGNMENTS

RESULT 1

I37027
protamine p1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 04-Oct-1996
C:Accession: I37027
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-

A:Reference number: I37013; MUID:94040810
A:Accession: I37027
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-6 <RES>

A:Molecule type: DNA
A:Cross-references: EMBL:Z12145; NID:g22910; PID:g579612

Query Match 42.5%; Score 17; DB 2: Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYR 4

DB 3 RYR 5

RESULT 2

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 30.0%; Score 12; DB 2: Length 3;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YR 4

DB 2 YR 3

RESULT 3

I84439

protamine P1 - savannah baboon (fragment)
C:Species: Papio hamadryas doguera (savannah baboon)
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 19-May-2000
C:Accession: I84439
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I84439
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12147; NID:g38134

Query Match 30.0%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ry 3
||
Db 3 ry 4

RESULT 4
I61883
protamine P1 - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 06-Sep-1996
C:Accession: I61883
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I61883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12146; NID:g38156

Query Match 30.0%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ry 3
||
Db 3 ry 4

RESULT 5
I37013
protamine P1 - Cercopithecus patas (fragment)
C:Species: Cercopithecus patas
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 07-Nov-1997
C:Accession: I37013
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I37013
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12150; NID:g22814

Query Match 30.0%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ry 3
||

Db 3 ry 4

RESULT 6
HOROHA
proctolin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01644
R:Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in inse
A:Reference number: A93048; MUID:76074708
A:Accession: A01644
A:Molecule type: Protein
A:Residues: 1-5 <SFA>
A:Note: the synthetic peptide had the same chromatographic, electrophoretic, and phar
R:O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A:Title: Pentapeptide (proctolin) associated with an identified neuron.
A:Reference number: A94260; MUID:81225865
A:Contents: annotation; biological source
C:Comment: This peptide is found in the lateral white neurons, which occur (in the co
innervate the striated hindgut muscles in insects and stimulate contraction of these
C:Superfamily: proctolin
C:Keywords: neuropeptide

Query Match 30.0%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ry 3
||
Db 1 ry 2

RESULT 7
B37325
pap fimbrial regulatory protein papI - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C:Accession: B37325
R:Braaten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
J. Bacteriol. 173, 1789-1800, 1991
A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus
A:Reference number: A37325; MUID:91154136
A:Accession: B37325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <BRA>
A:Cross-references: GB:M63747

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ey 6
||
Db 3 ey 4

RESULT 8
I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundv, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735

A;Accession: I39964
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M99041; NID:gl43471
C;Genetics:
A;Gene: rpsD

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 3
||
Db 3 RY 4

RESULT 9
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C;Species: Bacillus licheniformis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C;Accession: I39966
R;Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A;Reference number: I39966
A;Accession: I39966
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M99043; NID:gl43475
C;Genetics:
A;Gene: rpsD

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 3
||
Db 3 RY 4

RESULT 10
I39965
ribosomal protein S4 - Bacillus megaterium (fragment)
C;Species: Bacillus megaterium
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C;Accession: I39965
R;Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A;Reference number: I39963; MUID:93015735
A;Accession: I39965
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M99042; NID:gl43473
C;Genetics:
A;Gene: rpsD ----

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 3
||
Db 3 RY 4

RESULT 11
F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: F22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601
A;Accession: F22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YR 4
||
Db 4 YR 5

RESULT 12
A60411
proctolin - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60411
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt
Peptides 11, 205-211, 1990
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab
A;Reference number: A60411; MUID:90287800
A;Accession: A60411
A;Molecule type: protein
A;Residues: 1-5 <GRO>
C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horseshoe crab
C;Keywords: neuropeptide

Query Match 30.0%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 3
||
Db 1 RY 2

RESULT 13
A41946
T-cell receptor gamma chain (1t.22) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: A41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma chain
A;Reference number: A41946; MUID:92049316
A;Accession: A41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YR 4

Db 1 11
1 YR 2

RESULT 14

F37196

bradykinin-potentiating peptide 6 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C:Accession: F37196

R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

A:Reference number: A37196; MUID:90351557

A:Accession: F37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

27.5%; Score 11; DB 2; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1

|

Db 3 W 3

RESULT 15

A34626

RPCH-related neuropeptide - ferruginous spindle

C:Species: Fusinus ferrugineus (ferruginous spindle)

C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C:Accession: A34626

R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.

A:Reference number: A34626; MUID:90179762

A:Accession: A34626

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <KUR>

C:Keywords: neuropeptide

Query Match

27.5%; Score 11; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1

|

Db 4 W 4

Search completed: November 8, 2000, 07:28:01

Job time: 83 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:27:33 ; Search time 8.4 Seconds
(without alignments)
22.820 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Description
1	12	30.0	5 1 FARP_ARTTR
2	12	30.0	5 1 PRC2_PERAM
3	11	27.5	5 1 BPF7_BOTIN
4	11	27.5	5 1 U01_MOUSE
5	11	27.5	6 1 LOK1_LOCM1
6	9	22.5	4 1 FARP_HIRME
7	9	22.5	6 1 FARP_MONEX
8	9	22.5	6 1 OVM_LEPDE
9	8	20.0	4 1 FARP3_HIRME
10	8	20.0	4 1 FLRF_HIRME
11	8	20.0	4 1 FMRP_MACNI
12	7	17.5	5 1 ALI4_CARMA
13	7	17.5	5 1 BI0B_SALTY
14	7	17.5	6 1 ACPI_RABIT
15	5	12.5	4 1 E0SI_HUMAN
16	5	12.5	4 1 TUPT_HUMAN
17	5	12.5	5 1 TRM3_ECOLI
18	5	12.5	5 1 UC22_MAIZE
19	5	12.5	6 1 UN06_CLOPA
20	4	10.0	3 1 GRWM_HUMAN
21	4	10.0	3 1 LUXE_VIBFI
22	4	10.0	3 1 THYL_PIG
23	4	10.0	4 1 ACH1_ACHFU
24	3	7.5	5 1 PAR2_FARMA
25	3	7.5	5 1 SUGA_ACHDO
26	3	7.5	5 1 TPIS_CANFA
27	3	7.5	6 1 CIP1_MYTED
28	3	7.5	6 1 CIP2_MYTED
29	2	5.0	4 1 DCML_PSECH
30	2	5.0	4 1 DCMS_PSECH
31	2	5.0	5 1 B10A_CITFR
32	2	5.0	5 1 B10A_SALTY
33	2	5.0	5 1 BI0B_CITFR

34 2 5.0 5 1 UX44_CHLTR
35 2 5.0 6 1 TMOF_SARBU
36 2 5.0 6 1 TRPI_PSEPU
37 2 5.0 6 1 VP19_HSVIK
38 0 0.0 4 1 RM01_YEAST

P38005 chlamydia t
P41495 sarcophaga
P36414 pseudomonas
P23210 herpes simp
P36515 saccharomyc

ALIGNMENTS

RESULT 1
FARP_ARTTR
ID FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE RYIRF-AMIDE.
OS Artiopesthia triangulata.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Tricladida;
OC Terricola; Geoplanidae; Artiopesthia.
RN [1]
RP SEQUENCE AND SYNTHESIS.
RX MEDLINE; 94211927.
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 754 MW; 69D4004B4600000 CRC64;

Query Match 30.0%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ry 3
DB 1 ry 2

RESULT 2
PRCT_PERAM
ID PRCT_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE PROCTOLIN.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
RN [1]
RP SEQUENCE.
RC SPECIES-P.AMERICANA;
RX MEDLINE; 76074708.
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES-P.AMERICANA;
RX MEDLINE; 81225865.
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]

Db 5 W 5

RESULT 6

FAR4_HIRME STANDARD; PRT; 4 AA.

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRFAMIDE-LIKE NEUROPEPTIDE YMRP-AMIDE.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

RN [1]

RP SEQUENCE; 92195954.

RX MEDLINE; 93312289.

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of Rfamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 4 4

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match

Best Local Similarity 22.5%; Score 9; DB 1; Length 4;

Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 yrey 6

Db 1 YMRP 4

RESULT 7

FARP_MONEX

ID FARP_MONEX STANDARD; PRT; 6 AA.

AC P41966;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE FMRFAMIDE-LIKE NEUROPEPTIDE GNFRF-AMIDE.

OS Moniezia expansa (Sheep tapeworm).

OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Cestoda; Eucestoda;

OC Cyclophyllida; Anoplocephalidae; Moniezia.

RN [1]

RP SEQUENCE.

RX MEDLINE; 93312289.

RA Maule A.G., Shaw C., Halton D.W., Thim L.;

RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from

RL the sheep tapeworm, Moniezia expansa.";

RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 6 6

SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match

Best Local Similarity 22.5%; Score 9; DB 1; Length 6;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 wfy 3

Db 4 FRF 6

RESULT 8

OVM_LEPDE

ID OVM_LEPDE STANDARD; PRT; 6 AA.

AC P42985;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE OVIDUCTAL MOTILITY STIMULATING PEPTIDE (LED-OVM).

OS Leptinotarsa decemlineata (Colorado potato beetle).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;

OC Cucujiformia; Chrysomelidae; Chrysomelinae; Leptinotarsa.

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE-HEAD;

RX MEDLINE; 91271080.

RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,

RA Proost P., Torrekens S., de Loof A.;

RT "Isolation, identification and synthesis of novel oviductal motility

RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa

RL decemlineata.";

RL Peptides 12:31-36(1991).

CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE

CC OVIDUCT.

KW Neuropeptide; Amidation.

FT MOD_RES 6 6

SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match

Best Local Similarity 22.5%; Score 9; DB 1; Length 6;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 yr 4

Db 3 YK 4

RESULT 9

FAR3_HIRME

ID FAR3_HIRME STANDARD; PRT; 4 AA.

AC P42562;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

RN [1]

RP SEQUENCE.

RX MEDLINE; 92195954.

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of Rfamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 4 4

SQ SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match

Best Local Similarity 20.0%; Score 8; DB 1; Length 4;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ry 3

Db 3 RF 4

RESULT 10

FLRF_HIRME

ID FLRF_HIRME STANDARD; PRT; 4 AA.

AC P42561;

DT 01-NOV-1995 (Rel. 32, Created)

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FLRFAMIDE.
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
RN [1]
RP SEQUENCE.
RC SPECIES=H.MEDICINALIS;
RX MEDLINE; 92195954.
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamidae neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX MEDLINE; 94286417.
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CARDIAC CONTRACTION.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR PIR; A01426; ECNK.
DR PIR; A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
AMIDATION.

Query Match 20.0%; Score 8; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 3
DB 3 RF 4

RESULT 11
FMRF_MACNI
ID FMRF_MACNI STANDARD; PRT; 4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRFAMIDE (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS Macrocallista nimbosa (Sun-ray clam), Nerereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Veneroidea; Veneridae; Macrocallista.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC SPECIES=M.NIMBOSA; TISSUE=CEREBRAL PEDAL, AND VISCERAL GANGLION;
RX MEDLINE; 77215956.
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RC SPECIES=M.NIMBOSA; TISSUE=GANGLION;
RX MEDLINE; 78012038.
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
from the central ganglia of a bivalve mollusc.";
RL prep. Biochem. 7:261-281(1977).
RN [3]
RP SEQUENCE.
RC SPECIES=N.VIRENS;
RX MEDLINE; 90259866.
RA Krajniak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nerereis virens.";
RL Peptides 11:75-77(1990).
RN [4]
RP SEQUENCE.

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RC SPECIES=H.MEDICINALIS;
RX MEDLINE; 92195954.
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamidae neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [5]
RP SEQUENCE.
RC SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX MEDLINE; 94286417.
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CARDIAC CONTRACTION.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR PIR; A01426; ECNK.
DR PIR; A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;
AMIDATION.

Query Match 20.0%; Score 8; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 3
DB 3 RF 4

RESULT 12
AL14_CARMA
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
RX MEDLINE; 98121193.
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
AMIDATION (POTENTIAL).

Query Match 17.5%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 Y 3
DB 1 Y 1

RESULT 13
BI0B_SALTU

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ID BIOB_SALTY STANDARD; PRT; 5 AA.
AC P12678;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
GN BIOT.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 8906280.
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M21923; CAB25182.1; -.
DR STYGENE; SGI0027; BIOT.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER 5
SQ SEQUENCE 5 AA; 611 MW; 7761F40DD6F00000 CRC64;

Query Match 17.5%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ry 3
DB 3 RH 4

RESULT 14
ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACYLAMINO-ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
DE (APH) (ACYLAMINOACYL-PEPTIDASE) (FRAGMENT).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RX TISSUE=MUSCLE;
RX MEDLINE; 92222120.
RA Krishna R.G., Chin C.C.Q., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acetylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
CC ACID + PEPTIDE.

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CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
DR INTERPRO; IPR002471;
DR PROSITE; PS00708; PRO-ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 17.5%; Score 7; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 8.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 re 5
DB 3 RQ 4

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RESULT 15
EOSI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE EOSINOPHILOTACTIC PEPTIDES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76078412.
RA Goetzi E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilotactic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR PIR; A03190; ETHUL.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

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Query Match 12.5%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 e 5
DB 4 E 4

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Search completed: November 8, 2000, 07:29:14
Job time: 101 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:27:13 ; Search time 17.52 Seconds
(without alignments)
31.977 Million cell updates/sec

Title: 09-258947-1
Perfect score: 40
Sequence: 1 wryrey 6

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_14:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	11	27.5	6	13 P82096	P82096 litoria rub
2	8	20.0	5	13 P82071	P82071 litoria rub
3	8	20.0	5	13 P82072	P82072 litoria rub
4	5	12.5	5	13 P82070	P82070 litoria rub
5	5	12.5	6	10 P82181	P82181 spinacia ol
6	5	12.5	6	10 P82182	P82182 spinacia ol
7	4	10.0	5	10 Q99007	Q99007 hordeum vul
8	3	7.5	5	13 P82073	P82073 litoria rub
9	3	7.5	5	13 P82099	P82099 litoria rub
10	3	7.5	5	13 P82100	P82100 litoria rub
11	3	7.5	6	4 Q08720	Q08720 homo sapien
12	2	5.0	4	11 Q08433	Q08433 rattus norv

ALIGNMENTS

RESULT 1
P82096

ID P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoides; Hylidae; Litoria.
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 27.5%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
Db 5 w 5

RESULT 2
P82071 PRELIMINARY; PRT; 5 AA.
ID P82071;
AC P82071;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoides; Hylidae; Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians".
RL Aust. J. Chem. 49:953-963(1996).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 20.0%; Score 8; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ey 6
Db 2 EF 3

RESULT 3
P82072 PRELIMINARY; PRT; 5 AA.
ID P82072

AC P82072;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE RUBELLIDIN 3.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 20.0%; Score 8; DB 13; Length 5;
 Best Local Similarity 50.0%; Pred. No. 3e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ey 6
 I:
 2 EF 3

Db

RESULT 4
 P82070
 ID P82070 PRELIMINARY; PRT; 5 AA.
 AC P82070;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE RUBELLIDIN 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 12.5%; Score 5; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 3e+05;
 Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ey 6
 I:
 2 DF 3

Db

RESULT 5
 P82181
 ID P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Caryophyllales; Caryophyllales;
 OC Chenopodiaceae; Spinacia.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "Identification of all the proteins in the large subunit of an
 RT organelle (chloroplast) ribosome.";
 RL J. Biol. Chem. 0:0-0(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR INTERPRO: IPR002363; .
 DR PROSITE: PS01109; RIBOSOMAL_L10; 1.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 12.5%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 r 2
 I:
 4 R 4

Db

RESULT 6
 P82182
 ID P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Caryophyllales; Caryophyllales;
 OC Chenopodiaceae; Spinacia.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "Identification of all the proteins in the large subunit of an
 RT organelle (chloroplast) ribosome.";
 RL J. Biol. Chem. 0:0-0(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR INTERPRO: IPR002363; .
 DR PROSITE: PS01109; RIBOSOMAL_L10; 1.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 12.5%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 Y 3 Query Match 5.0%; Score 2; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 F 1
QY 2 r 2
Db 4 K 4

Search completed: November 8, 2000, 07:29:00
Job time: 107 sec

RESULT 11
Q08720 PRELIMINARY; PRT; 6 AA.
AC Q08720;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93010691.
RA Waechter G., Habener J.F.;
RT "Novel testis germ cell-specific transcript of the CREB gene contains
an alternatively spliced exon with multiple in-frame stop codons.";
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 7.5%; Score 3; DB 4; Length 6;
Best Local Similarity 0.0%; Pred. No. 3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 Y 3
Db 3 F 3

RESULT 12
Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOAL (EC 2.4.1.17) (UDPGT)
(FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-GUNN;
RX MEDLINE; 91282758.
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR
CC -1- BETA-D-GLUCONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROsome.
DR EMBL; S38636; AAB19259.1; -.
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1
FT NON_TER 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:25:43 ; Search time 14.65 Seconds
(without alignments)
14.004 Million cell updates/sec

Title: 09-258947-1

Perfect score: 40

Sequence: 1 wryrey 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 26426

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	67.5	6	21	Y51556
2	23	57.5	5	19	W87121
3	23	57.5	5	20	W94177
4	23	57.5	6	6	P50103
5	23	57.5	6	17	R90503
6	23	57.5	6	18	W23193
7	23	57.5	6	18	W21070
8	23	57.5	6	20	Y55230
9	23	57.5	6	21	Y86976
10	23	57.5	6	21	Y50635
11	22	55.0	6	7	P61446
12	22	55.0	6	16	R67472
					Neuropeptide Y inh
					Peptide determined
					FG loop sequence o
					Cyclic peptide wit
					Hybridoma ATCC HB-
					Terminal peptide e
					Lipolytic enzyme o
					ATCC HB 11884 mono
					Human haematopoiet
					Alphal-proteinase
					Luteinising hormon
					Mu opioid receptor

13	20	50.0	3	15	R42556	ACE inhibitor SP3.
14	20	50.0	4	19	W20416	Human microtubule
15	20	50.0	4	19	W43233	Peptide #10 having
16	20	50.0	5	18	W12486	Interleukin-6 anta
17	20	50.0	5	19	W87123	Peptide determined
18	20	50.0	5	21	Y51555	Neuropeptide Y inh
19	20	50.0	6	18	W28887	Oploid peptide. S
20	20	50.0	6	18	W22296	von Willebrand fac
21	20	50.0	6	18	W23134	Cyclic somatostati
22	20	50.0	6	18	W23136	Cyclic somatostati
23	20	50.0	6	18	W23116	Cyclic somatostati
24	20	50.0	6	18	W23117	Cyclic somatostati
25	20	50.0	6	18	W23129	Cyclic somatostati
26	20	50.0	6	18	W23130	Cyclic somatostati
27	20	50.0	6	18	W23131	Cyclic somatostati
28	20	50.0	6	18	W23132	Cyclic somatostati
29	20	50.0	6	18	W23107	Cyclic somatostati
30	20	50.0	6	18	W23108	Cyclic somatostati
31	20	50.0	6	18	W23109	Cyclic somatostati
32	20	50.0	6	18	W23110	Cyclic somatostati
33	20	50.0	6	18	W23111	Cyclic somatostati
34	20	50.0	6	18	W23112	Cyclic somatostati
35	20	50.0	6	18	W23102	Cyclic somatostati
36	20	50.0	6	18	W23103	Cyclic somatostati
37	20	50.0	6	18	W23106	Cyclic somatostati
38	20	50.0	6	18	W23093	Cyclic somatostati
39	20	50.0	6	18	W23094	Cyclic somatostati
40	20	50.0	6	18	W23095	Cyclic somatostati
41	20	50.0	6	18	W23096	Cyclic somatostati
42	20	50.0	6	18	W23097	Cyclic somatostati
43	20	50.0	6	18	W23098	Cyclic somatostati
44	20	50.0	6	18	W23099	Cyclic somatostati
45	20	50.0	6	18	W23091	Cyclic somatostati

ALIGNMENTS

RESULT 1

Y51556
ID Y51556 standard; peptide; 6 AA.
XX
AC Y51556;
XX
DT 18-MAY-2000 (first entry)
XX
DE Neuropeptide Y inhibitory peptide #6.
XX
KW Neuropeptide Y; side effect; addiction; blood pressure; libido;
KW appetite suppressor; cardiovascular function; circadian rhythm;
KW hypertension.
XX
OS Synthetic.
XX
PN US6013633-A.
XX
PD 11-JAN-2000.
XX
PF 07-AUG-1997; 97US-0907403.
XX
PR 07-AUG-1997; 97US-0907403.
XX
XX (UYCI-) UNIV CINCINNATI.
XX
PA Balasubramaniam A, Chance WT;
XX
PI Hybridoma ATCC HB-
XX
DR Terminal peptide e
XX
XX Lipolytic enzyme o
XX
XX ATCC HB 11884 mono
XX
XX Human haematopoiet
XX
XX Alphal-proteinase
XX
XX Luteinising hormon
XX
XX Mu opioid receptor

CC This invention describes a novel method for the suppression of
 CC neuropeptide-Y (NPY) mediated physiological response which comprises
 CC the administration of tripeptide derivatives (I) with less side effects
 CC and lower risk of addiction than prior art. (I) is useful for suppression
 CC of a NPY-mediated physiological response, preferably lowering of blood
 CC pressure, suppressing the appetite, augmenting the libido, stimulating
 CC cardiovascular function, modulation of circadian rhythm and particularly
 CC for treatment of hypertension. (I) avoids the side effects and the risk
 CC of addiction associated with prior art treatments such as amphetamines.
 CC Y51549-Y51556 represent peptides capable of suppressing neuropeptide Y
 CC activity.
 CC
 XX Sequence 6 AA;

SQL

Query Match 67.5%; Score 27; DB 21; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.1e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 wryrey 6
 | | | |
 Db 1 wrywry 6

RESULT 2

ID W87121
 XX W87121 standard; peptide; 5 AA.

AC W87121;

DT 09-FEB-1999 (first entry)

XX Peptide determined by the method of the invention.

DE Amino acid determination; molecular mass; fragmentation spectrum;

KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.

XX Synthetic.

XX GB2325465-A.

XX 25-NOV-1998.

PD 22-MAY-1998; 98GB-0011196.

PF 22-MAY-1997; 97GB-0010582.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

FA Parekh RB, Prime SB, Townsend RR, Wedd NS;

XX WPI; 1998-571195/49.

PT Peptide sequence determination used in e.g. DNA cloning - by
 PT comparing mass spectra of the unknown peptide with a library of
 PT linear chain known peptide sequences

XX Example 1; Page 20; 40pp; English.

CC The invention relates to a method for determination of the amino acid
 CC sequence of an unknown peptide. The method comprises (a) determining
 CC the molecular mass and an experimental fragmentation spectrum for the
 CC peptide; (b) comparing the experimental fragmentation spectrum of the
 CC unknown peptide with a theoretical fragmentation spectra calculated for
 CC a peptide library composed of all possible linear sequences of amino
 CC acids having a total mass that corresponds to the molecular mass of the
 CC unknown peptide; and (c) identifying a peptide in the library with a
 CC theoretical fragmentation spectrum that most closely matches the
 CC fragmentation spectrum of the unknown peptide. The method is useful in
 CC DNA cloning, anti-body production, identification of recombinant
 CC products, and the study of post-translational modifications. It allows
 CC the sequence of unknown peptides or proteins with no sub-sequence
 CC identity, to be characterised using mass spectrometry. Sequences W87101

CC to W87364 represent a library of linear peptides constructed to exemplify
 CC the method. The isoleucine residue in these peptides can be replaced by
 CC leucine to construct another 264 linear peptides to be included in the
 CC library.
 CC
 XX Sequence 5 AA;

Query Match 57.5%; Score 23; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryr 4
 | | |
 Db 2 whyr 5

RESULT 3

ID W94177
 XX W94177 standard; peptide; 5 AA.

AC W94177;

DT 14-APR-1999 (first entry)

XX FG loop sequence of fluorescein-binding monobody clone pLB25.4.

DE Fibronectin type III; Fn3; monobody; beta-strand domain; loop region;

KW specific binding partner; SBP; catalysis; LRS; fluorescein.

XX Unidentified.

XX WO9856915-A2.

XX 17-DEC-1998.

PF 12-JUN-1998; 98WO-US12099.

PR 12-JUN-1997; 97US-0049410.

XX (RESE) RESEARCH CORP TECHNOLOGIES INC.

XX Koide S;

XX WPI; 1999-060331/05.

PT Production of antibody compounds, particularly catalytic antibodies
 PT - using a fibronectin type III molecular scaffolding comprising
 PT beta-strand domain sequences and modified in one or more loop
 PT sequences

XX Example 12; Page 43; 96pp; English.

CC The invention relates to a synthetic fibronectin type III (Fn3)
 CC polypeptide monobody that comprises Fn3 beta-strand domain sequences
 CC that are linked to loop region sequences (LRSs). One or more of the loop
 CC sequences in the synthetic Fn3 vary by deletion, insertion, or
 CC replacement of at least 2 amino acids from the corresponding LRSs in
 CC wild-type Fn3. Host cells containing an expression vector comprising the
 CC synthetic Fn3 nucleic acid are used for the production of the Fn3
 CC monobody. The invention also provides methods of identifying the amino
 CC acid sequence of a polypeptide molecule (1) capable of binding to a
 CC specific binding partner (SBP) so as to form a polypeptide:SBP complex;
 CC (1i) capable of catalysing a chemical reaction with a catalysed rate
 CC constant, Kcat, and an uncatalysed rate constant, Kuncat, such that the
 CC ratio of the Kcat/Kuncat is greater than 10. Sequences W94175-77
 CC represent FG loop sequences of fluorescein-binding monobody clones from
 CC library #4.

XX Sequence 5 AA;

Query Match 57.5%; Score 23; DB 20; Length 5;

Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryr 4
Db 2 wrwr 5

RESULT 4 --

P50103
ID P50103 standard; Protein; 6 AA.

XX AC P50103;

XX 16-OCT-1991 (first entry)

XX Cyclic peptide with alpha-amylase-inhibitor activity.

XX Alpha-amylase-inhibitor; cyclic peptide.

XX Streptomyces aureofaciens.

XX Key Location/Qualifiers

XX Misc-difference 6 /label= 5-25 natural AA

XX EP151246-A.

XX 14-AUG-1985.

XX 22-NOV-1984; 84EP-0114064.

XX 21-JAN-1984; 84DE-3402021.

XX (PARH) HOECHST AG.

XX Vertesy L, Tripier D, Ritzel H;

XX WPI; 1985-197969/33.

XX New cyclic peptide(s) - useful as alpha-amylase inhibitors.

XX Example; p17; 20pp; German.

XX The new cyclic peptide is useful as an alpha-amylase-inhibitor,
XX and may be used in the treatment of diabetes, prediabetes and
XX obesity, and for preventing dental caries.

XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wry 3
Db 3 wry 5

RESULT 5

R90503
ID R90503 standard; peptide; 6 AA.

XX AC R90503;

XX 03-SEP-1996 (first entry)

XX Hybridoma ATCC HB-11884 antibody displacing peptide #1.

XX Antibody; displacement; cell separation system; cell surface antigen; Ag;
XX random peptide display library; complementarity determining region; CDR;
XX antibody; Ab; peptide; CD34 cell; haematopoietic cell; tumour cell;

KW Lymphocyte; high dose therapy; immune system; chemotherapy;
XX patient-specific vaccine.

OS Synthetic.

XX WO9534817-A1.

XX 21-DEC-1995.

XX 13-JUN-1995; 95WO-US07491.

XX 14-JUN-1994; 94US-0259427.

XX (BAXT) BAXTER INT INC.

XX Al-abdaly FA, Deans RJ, Guillermo R, Helgeson SL;

XX Kobori JA, Tseng-law J;

XX WPI; 1996-049806/05.

XX Selecting target cells by reacting specific antibody to surface
XX antigen - then disrupting the complex formed with peptide displacer,
XX partic. for selecting CD34 cells for reconstitution of immune system
XX after anticancer treatment

XX Claim 27; Page 158; 170pp; English.

XX R90503-R90511 represent antibody displacing peptides. These sequences
XX displace the antibody produced by the hybridoma ATCC HB-11884 (9187).
XX These sequences can be used in a method to select target cells from a
XX heterogeneous cell suspension. In the suspension, there is at least one
XX complex of a cell separation system, linked to a primary antibody (Ab)
XX which is bound to the cell surface antigen (Ag). The complex is
XX separated from the rest of the suspension, and contacted with a peptide
XX (such as this sequence) that binds to the Ab, displacing it from the Ag
XX and releasing the cell. These sequences can be identified by biopanning
XX random peptide display libraries with the Ab, by analysis of potential
XX antigenic peaks of the cell surface antigen, or by analysis of the
XX complementarity determining regions of the Ab. These sequences can also
XX be used in a method for determining the number of specific cells in a
XX composition. The methods can be used for positive selection of CD34
XX haematopoietic cells, and removal of undesired tumour cells or
XX lymphocytes from the selected cells. The pure CD34 cells are reinfused
XX into a cancer patient after high dose therapy to reconstitute the immune
XX system. Cancer cells can also be isolated to determine their
XX chemotherapeutic susceptibility, or for the production of
XX patient-specific vaccines or antibodies. These sequences allow for the
XX recovery of cells from solid supports, in high yield, without enzymatic
XX cleavage. They are relatively inexpensive and safe, and leave cell
XX surface proteins intact.

XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 17; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryr 4
Db 2 wrwr 5

RESULT 6

W23193

ID W23193 standard; peptide; 6 AA.

XX AC W23193;

XX 28-OCT-1997 (first entry)

XX Terminal peptide extension for lipolytic enzyme.

KW Lipolytic enzyme; modification; peptide extension; detergent;
 KW washing powder; dishwashing composition; pitch removal; paper;
 KW pulp; manufacture; degreasing; hide; sheepskin; wool; catalysis;
 KW organic synthesis; transesterification; esterification;
 KW ester hydrolysis; baking; defatting.
 XX
 OS Synthetic.
 XX
 PN WO9704078-A1.
 XX
 PD 06-FEB-1997.
 XX
 XX 12-JUL-1996; 96WO-DK00321.
 XX
 PR 01-APR-1996; 96DK-0000372.
 PR 14-JUL-1995; 95DK-0000832.
 PR 13-SEP-1995; 95DK-0001013.
 PR 29-SEP-1995; 95DK-0001096.
 PR 21-NOV-1995; 95DK-0001306.
 PR 14-FEB-1996; 96US-0011634.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 XX Fuglsang CC, Halkier T, Jorgensen ST, Okkels JS;
 PI Patkar SA, Pertersen DA, Thellersen M, Vind J;
 XX
 XX WPI; 1997-132621/12.
 XX
 PT Modified lipolytic enzymes with peptide extensions at one or both
 PT ends - esp. for use in detergent and dishwashing compsn., have
 PT improved substrate affinity, stability and wash performance
 XX
 XX Claim 12; Page 179; 197pp; English.
 PS
 CC A lipolytic enzyme, modified by a peptide extension, e.g. the
 CC present sequence, of its carboxy and/or amino terminus, can be used
 CC in detergents, particularly in washing powders or dishwashing
 CC compositions. It may also be used to remove pitch in paper and
 CC pulp manufacture, to degrease hides, sheepskins and wool, to
 CC catalyse organic synthesis, e.g. (transesterification or ester
 CC hydrolysis, in baking and in other degreasing/defatting processes.
 CC The peptide extension(s) increases substrate affinity, confers
 CC stability and especially improves wash performance, i.e. better
 CC lipid soil removal, reducing the amount of enzyme used.
 XX
 SQ Sequence 6 AA;
 Query Match 57.5%; Score 23; DB 18; Length 6;
 Best Local Similarity 75.0%; Pred. NO. 2.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wryr 4
 Db 1 wrwr 4
 RESULT 7
 W21070
 ID W21070 standard; peptide; 6 AA.
 XX
 AC W21070;
 XX
 DT 19-JUN-1997 (first entry)
 XX
 DE Lipolytic enzyme opt. N- or C-terminal extension peptide #38.
 XX
 KW Lipolytic enzyme; detergent; lard; cotton swatch; laundry;
 KW dishwashing.
 XX
 OS Synthetic.
 XX
 PN WO9707202-A.
 XX

XX 27-FEB-1997.
 PD
 XX 12-AUG-1996; 96WO-DK00341.
 XX
 PR 07-MAY-1996; 96US-0016754.
 PR 11-AUG-1995; 95DK-0000905.
 PR 29-SEP-1995; 95DK-0001096.
 PR 14-FEB-1996; 96US-0011627.
 PR 01-APR-1996; 96DK-0000374.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 XX Borch K, Kretschmar T, Okkels JS, Patkar SA, Petersen DA;
 PI Royer JC, Svendsen A, Thellersen M;
 XX
 DR WPI; 1997-165287/15.
 XX
 PT Lipolytic enzyme with high capacity to remove lard in one wash cycle -
 PT also related DNA, vectors and transformed cells, useful in laundry and
 PT dishwashing formulations
 XX
 PS Claim 17; Page 245; 274pp; English.
 XX
 CC The sequences given in W21033-92 are peptides which may be added to
 CC the N- or C-terminal of the lipolytic enzyme of the invention. The
 CC lipolytic enzyme, when present in a specified detergent composition,
 CC is able to remove at least 15% more lard from soiled cotton swatches,
 CC (9 by 9 cm) than an equiv. enzyme-free compsn. in a one-cycle wash
 CC assay. The assay uses 7 lard-stained cotton swatches in 1000 ml
 CC water (3.2 mM Ca2+/Mg2-, ratio 5:1; 5 g/l detergent; pH 10 plus 12500 LU
 CC of enzyme/l) for 20 min at 30 deg.C, in a thermostated Terg-O-to-Meter,
 CC then 15 min rinsing, drying overnight and soxhlet extn. and
 CC quantification of fatty material. The enzyme may be used in laundry
 CC and dishwashing formulations. It is able to remove a substantial
 CC amount of lard in a single cycle under realistic washing conditions.
 XX
 SQ Sequence 6 AA;
 Query Match 57.5%; Score 23; DB 18; Length 6;
 Best Local Similarity 75.0%; Pred. NO. 2.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wryr 4
 Db 1 wrwr 4
 RESULT 8
 Y55230
 ID Y55230 standard; peptide; 6 AA.
 XX
 AC Y55230;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE ATCC HB 11884 monoclonal antibody 9187 releasing peptide SEQ ID NO:124.
 XX
 KW Antibody releasing peptide; CD34; hybridoma; binding; antigen;
 KW cell surface antigen; identification; haematopoietic stem cell;
 KW tumour; cancer; immune system; therapy; displacement.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN US5968753-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 07-JUN-1995; 95US-0482228.
 XX
 PR 14-JUN-1994; 94US-0259427.
 XX

XX (NEXE-) NEXELL THERAPEUTICS INC.
 XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX WPI; 1999-590399/50.
 XX Short peptides useful for displacing antibodies from cell surface
 PT antigens.
 XX Claim 9; Column 148; 81pp; English.
 XX The present invention describes peptides of 4-17 amino acids which
 CC displace either the anti-CD34 monoclonal antibody designated 561, the
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC
 CC HB-11646 (designated 9069), the anti-CD34 antibody produced by
 CC hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer
 CC antibody produced by hybridoma ATCC HB-11884 (9187), from a cell
 CC surface antigen on a target cell. The peptides are useful for
 CC displacing antibodies bound to cell surfaces to release cells that
 CC have been positively selected by antibody-mediated binding to beads
 CC or other solid support. Y55107 to Y55319 represent peptides used in
 CC the exemplification of the present invention.
 XX Sequence 6 AA;
 SQ

Query Match 57.5%; Score 23; DB 20; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryr 4
 Db 2 wrwr 5

RESULT 9
 Y86976
 ID Y86976 standard; Peptide; 6 AA.
 XX Y86976;
 AC
 XX 09-MAY-2000 (first entry)
 DT
 XX Human haematopoietic CD34+ cell binding peptide SEQ ID #124.
 DE
 XX Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;
 KW non-enzymatic cell selection method; haematopoietic stem cell;
 KW haematopoietic progenitor cell; antibody 561; breast cancer cell;
 KW antibody 9187; cell surface determinant; diagnostic cell based assay.
 XX
 OS Homo sapiens.
 XX
 XX US6017719-A.
 PN
 XX 25-JAN-2000.
 PD
 XX 07-JUN-1995; 95US-0482528.
 PF
 XX 14-JUN-1994; 94US-0259427.
 PR
 XX (NEXE-) NEXELL THERAPEUTICS INC.
 PA
 XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX WPI; 2000-136676/12.
 DR
 XX Non-enzymatic method for the positive selection of target cells from a
 PT heterogeneous cell suspension, useful for selecting human breast cancer
 PT cells from a patient's blood or bone marrow -

PS Example 17; Column 21; 82pp; English.
 XX This sequence represents a human haematopoietic CD34+ cell binding
 CC peptide, and was used to test the method of the invention: The method is
 CC a non-enzymatic method for the positive selection of one or more target
 CC cells from a heterogeneous cell suspension, by using specific peptides
 CC which effect the displacement and release of a specific target cell
 CC from a specific monoclonal antibody. The method is useful for positive
 CC selection and specific release of target human haematopoietic
 CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and
 CC the antibody 561. The method is also useful for positive selection and
 CC specific release of target human breast cancer cells, bound by the
 CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or
 CC bone marrow. Identification of peptide epitopes for antibodies which
 CC recognise cell surface determinants also allows construction of
 CC diagnostic cell based assays. The peptide mediated release is enzyme free
 CC and thus leaves the cell surface proteins intact. Moreover, peptide
 CC mediated release leaves the target cell free of bound antibody or
 CC antibody fragments. The method also produces a high yield of functional
 CC target cells and is relatively inexpensive to carry out.
 XX Sequence 6 AA;
 SQ

Query Match 57.5%; Score 23; DB 21; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wryr 4
 Db 2 wrwr 5

RESULT 10
 Y50635
 ID Y50635 standard; Peptide; 6 AA.
 XX Y50635;
 AC
 XX 01-FEB-2000 (first entry)
 DT
 XX Alpha-proteinase inhibitor peptide ligand 15.
 DE
 XX Alpha-proteinase inhibitor; AIPi; treatment; emphysema;
 KW genetic deficiency.
 KW
 XX Synthetic.
 OS
 XX US5985836-A.
 PN
 XX 16-NOV-1999.
 PD
 XX 31-JUL-1998; 98US-0127574.
 PF
 XX 31-JUL-1998; 98US-0127574.
 PR
 XX (FARB) BAYER CORP.
 PA
 XX Bastek PD, Lang JM, Carbonell RG, Baumbach GA;
 PI WPI; 2000-012806/01.
 DR
 XX Composition comprising a peptide used in the treatment of emphysema -
 PT Claim 1; Column 29-30; 27pp; English.
 XX This invention describes a novel composition comprising a peptide having
 CC an available alpha-1 proteinase inhibitor (AIPi) binding domain. The
 CC invention also includes novel method of purifying an alpha-1 proteinase
 CC inhibitor comprising contacting a solution containing the alpha-1
 CC proteinase inhibitor with a substrate such that binding occurs between
 CC the alpha-1 proteinase inhibitor and the substrate. The substrate
 CC comprises peptides (see Y50621-Y50682) bound to a support material. The

CC composition described in the invention can be used in the treatment of
 CC emphysema caused by genetic deficiency.

SQ Sequence 6 AA;

Query Match 57.5%; Score 23; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.le+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wryr 3
 |||
 Db 3 wryr 5

RESULT 11

P61446
 ID P61446 standard; protein; 6 AA.

XX AC P61446;

XX DT 04-AUG-1991 (first entry)

XX DE Luteinising hormone releasing hormone analogue.

XX KW Luteinising hormone releasing hormone; analogue; ovulation;
 XX KW endometriosis; spermatogenesis; prostatic cancer;

XX PN EP182262-A.

XX PD 28-MAY-1986.

XX PF 12-NOV-1985; 85EP-0114386.

XX PR 13-NOV-1984; 84US-0671153.

XX PA (SYNT) SYNTAX (USA) INC.

XX PI Nestor JJ, Vickery BH;

XX DR WPI; 1986-138714/22.

XX PT New peptide analogues{ of LHRH with antagonist activity - contg.
 residue of new haloalkyl-guanidino-substd. aminoacid.

XX PS Claim 8; page 39; 41pp; English.

XX CC The peptide is a LHRH analogue. The peptide antagonist is made more
 CC effective by the incorporation of a novel haloalkylguanidino-substd.
 CC amino acid at position 6. The analogue may be used for the inhibition
 CC of ovulation and treatment of endometriosis in females, and inhibition
 CC of spermatogenesis and the treatment of prostatic tumours. Daily doses
 CC are 0.01-10, pref. 0.01-5 mg/kg enterally, parenterally, transdermally or
 CC in sustained release form.

SQ Sequence 6 AA;

Query Match 55.0%; Score 22; DB 7; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.le+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 wryr 4
 |||
 Db 3 wsyr 6

RESULT 12

R67472
 ID R67472 standard; peptide; 6 AA.

XX AC R67472;

XX

DT 25-JUL-1995 (first entry)
 XX DE Mu opioid receptor antagonist NM 137.
 XX KW Mu opioid receptor antagonist; opiate analgesics; morphine;
 KW (3)H-[D-Ala(2),Mephe(4),Gly-ol(5)]-enkephalin; DAGO;
 KW binding inhibitor.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Misc-difference 1..6
 FT FT /note= "D-form residues"

FT FT Misc-difference 1

FT FT /label= acetylated

FT FT Misc-difference 6

FT FT /label= amidated

XX PN US5367053-A.

XX PD 22-NOV-1994.

XX PF 19-MAY-1993; 93US-0064517.

XX PR 19-MAY-1993; 93US-0064517.

XX DA (HOUG-) HOUGHTEN PHARM INC.

XX PI Dooley CT, Houghten RA;

XX DR WPI; 1995-005892/01.

XX PT New peptide opioid receptor antagonists - useful for research,
 FT drug screening and possibly therapeutic purposes

XX PS Claim 4; Fig 1B; 8pp; English.

XX CC R67472-R67492 are opioid receptor (OR) antagonists, specifically
 CC they inhibit the binding of (3)H-[D-Ala(2),Mephe(4),Gly-ol(5)]-
 CC enkephalin (DAGO) to mu ORs. They can be used to study OR subtypes
 CC and to screen cpds. for affinity to ORs. They may also be useful
 CC for blocking the side effects of opiate analgesics (such as
 CC morphine), in the treatment of constipation and pruritis.

XX SQ Sequence 6 AA;

Query Match 55.0%; Score 22; DB 16; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.le+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 wryr 4
 |||
 Db 3 wmyr 6

RESULT 13

R42556
 ID R42556 standard; peptide; 3 AA.

XX AC R42556;

XX DT 07-DEC-1994 (first entry)

XX DE ACE inhibitor SP3.

XX KW Angiotensin converting enzyme; ACE; inhibitor; SP5; SP4; SP3;
 KW hypertension; blood pressure.

XX OS Synthetic.

XX PN JP06065288-A.

XX

PD 08-MAR-1994.
 XX
 PF 19-AUG-1992; 92JP-0220270.
 XX
 PR 19-AUG-1992; 92JP-0220270.
 XX
 PA (APIA-) API KK.
 XX
 DR WPI; 1994-115194/14.
 XX
 PT New tri-, tetra- and penta-peptide(s), e.g. Trp-Lys-Tyr - are ACE
 PT inhibitors useful for treatment or prophylaxis of hypertension
 XX
 PS Claim 1; Page 2; 5pp; Japanese.
 XX
 CC Peptides SP3, SP4 and SP5 have ACE inhibiting activity. They can be
 CC prepd. easily and in high yield. They are useful for treatment or
 CC prophylaxis of hypertension.
 XX
 SQ Sequence 3 AA;
 Query Match 50.0%; Score 20; DB 15; Length 3;
 Best Local Similarity 66.7%; Pred. No. 2.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wry 3
 | : |
 Db 1 wky 3
 RESULT 14
 Y20416
 ID Y20416 standard; Protein; 4 AA.
 XX
 AC Y20416;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human microtubule associated protein 2 mutant fragment 112.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-IB00705.
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX
 DR WPI; 1998-609901/51.
 DR N-PSDB; X75757.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 RNA
 XX
 PS Disclosure; Figure 6; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 4 AA;
 Query Match 50.0%; Score 20; DB 19; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wry 3
 | : |
 Db 1 wky 3
 RESULT 15
 W43233
 ID W43233 standard; peptide; 4 AA.
 XX
 AC W43233;
 XX
 DT 31-MAR-1998 (first entry)
 XX
 DE Peptide #10 having anti-microbial activity.
 XX
 KW Anti-microbial peptide; bee sting; melittin; haemolytic activity;
 KW bee venom; red blood cell; cell lysis; inhibition; Escherichia Coli;
 KW trypsin; D-amino acid; IC50.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 4 /note= "fluorenylmethoxycarbonyl-modified lysine"
 FT Modified-site 4 /note= "Optionally D-form residue, C-terminal amide"
 XX
 PN US5698673-A.
 XX
 PD 16-DEC-1997.
 XX
 PF 04-MAY-1995; 95US-0434761.
 XX
 PR 18-JUN-1993; 93US-0079445.
 XX
 PA (TORR-) TORREY PINES INST.
 XX
 PI Blondelle SE, Houghten RA, Pinilla C;
 XX
 DR WPI; 1998-051545/05.

xx Anti-melittin peptide(s) - useful for treating bee stings
PT
xx Example 1; Column 17; 26pp; English.
PS
xx Peptides represented by the formula (KFmoc)WKX, where X is any L-or
CC D-amino acid and KFmoc is fluorenylmethoxycarbonyl-lysine, were
CC synthesised and screened for anti-microbial activity against Escherichia
CC coli. The present peptide showed anti-microbial activity with an IC50
CC value (concentration necessary to inhibit 50 per cent growth of bacteria)
CC of 27 microg/ml (with an L-form residue at position 4). The invention
CC provides peptides having anti-melittin activity with IC50 values of less
CC than 30 microg/ml which are useful for treating melittin poisoning.
CC Melittin is the active compound in bee venom and causes cell lysis.
CC Peptides having anti-melittin activity have one of the following
CC formulae: AC-IVILLZ2-NH2; AC-IVILT2-NH2; AC-IVILL2-NH2; AC-IVIEFF2-NH2;
CC AC-Z1-Z2-I-23-24-E-NH2; AC-MILWIE-NH2; AC-VIQQFV-NH2; AC-WIQIFI-NH2;
CC where Z= an optionally methylated or chlorinated D-form or natural amino
CC acid; Z1= F or I; Z2= I or Q; Z3= W or Y and Z4= C or F.
xx
SQ Sequence 4 AA;

Query Match 50.0%; Score 20; DB 19; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wry 3
I:I
Db 2 wky 4

Search completed: November 8, 2000, 07:27:28
Job time: 105 sec

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OM protein - protein search, using sw model

Run on: November 8, 2000, 07:26:03 ; Search time 11.72 Seconds
(without alignments)
8.581 Million cell updates/sec

Title: 09-258947-1

Perfect score: 40

Sequence: 1 wryrey 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 22255

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Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*

5: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	67.5	6	3	US-08-907-403A-8
2	23	57.5	6	2	US-08-482-228-124
3	23	57.5	6	2	US-09-127-574-15
4	23	57.5	6	3	US-08-482-528-124
5	21	52.5	6	1	US-08-014-979-81
6	20	50.0	5	1	US-08-240-511-1
7	20	50.0	5	3	US-08-907-403A-7
8	20	50.0	6	1	US-08-487-006-17
9	20	50.0	6	1	US-08-537-069-12
10	20	50.0	6	2	US-08-488-659A-17
11	19	47.5	3	1	US-08-305-768-27
12	19	47.5	3	2	US-08-871-163-27
13	19	47.5	3	3	US-08-767-903-27
14	19	47.5	3	4	PCT-US95-11724-27
15	19	47.5	4	1	US-08-165-545-7
16	19	47.5	4	1	US-08-256-771-16
17	19	47.5	4	1	US-08-381-984-16
18	19	47.5	4	3	US-08-105-904B-24
19	19	47.5	5	1	US-07-851-941-1
20	19	47.5	6	1	US-07-851-941-6
21	19	47.5	6	1	US-08-253-854-57
22	19	47.5	6	1	US-08-305-768-12
23	19	47.5	6	2	US-08-871-163-12
24	19	47.5	6	3	US-08-105-904B-19
25	19	47.5	6	3	US-08-767-903-12
26	19	47.5	6	4	PCT-US95-11724-12
27	18	45.0	4	2	US-08-592-646A-62
28	18	45.0	5	1	US-08-068-947-2

29 18 45.0 5 1 US-08-321-625-3
30 18 45.0 5 1 US-08-321-625-15
31 18 45.0 5 5 5185259-9
32 18 45.0 6 1 US-08-082-847-4
33 18 45.0 6 1 US-08-253-854-79
34 18 45.0 6 1 US-08-253-854-84
35 18 45.0 6 1 US-07-653-091A-8
36 18 45.0 6 1 US-08-338-890B-4
37 18 45.0 6 1 US-08-338-890B-5
38 18 45.0 6 1 US-08-485-068-8
39 18 45.0 6 2 US-08-481-598-8
40 18 45.0 6 2 US-08-660-747-21
41 18 45.0 6 2 US-08-660-747-26
42 18 45.0 6 2 US-08-660-747-27
43 18 45.0 6 2 US-08-660-747-52
44 18 45.0 6 2 US-08-660-747-53
45 18 45.0 6 2 US-08-660-747-54

ALIGNMENTS

RESULT 1

US-08-907-403A-8

; Sequence 8, Application US/08907403A

; Patent No. 6013633

; GENERAL INFORMATION:

; APPLICANT: Balasubramaniam, Ambikaipakan

; APPLICANT: Chance, William T.

; TITLE OF INVENTION: Compounds For Control

; TITLE OF INVENTION: Of Appetite, Blood Pressure, Cardiovascular

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wood, Heron & Evans, L.L.P.

; STREET: 441 Vine Street

; CITY: Cincinnati

; STATE: Ohio

; COUNTRY: USA

; ZIP: 45202-2917

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch,

; MEDIUM TYPE: 1.44 MB storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/907,403A

; FILING DATE: 07-AUG-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/023,588

; FILING DATE: 09-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Albainy-Jenel, Stephen R.

; REGISTRATION NUMBER: 41,487

; REFERENCE/DOCKET NUMBER: UOC-113A-111

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 241-2324

; TELEFAX: (513) 421-7269

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: no

; ANTI-SENSE: no

; US-08-907-403A-8

Query Match 67.5% Score 27; DB 3; Length 6;

Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 wryey 6
||| |
Db 1 WRWRY 6

RESULT 2

US-08-482-228-124
; Sequence 124, Application US/08482228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-228-124

Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
||| |
Db 2 WRWR 5

RESULT 3

US-09-127-574-15
; Sequence 15, Application US/09127574
; Patent No. 5985836
; GENERAL INFORMATION:
; APPLICANT: Bastek, Patrick
; APPLICANT: Lang, John M.
; APPLICANT: Baumbach, George A.
; APPLICANT: Carbonell, Ruben G.
; TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides

; FILE REFERENCE: MSB-7248
; CURRENT APPLICATION NUMBER: US/09/127,574
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-127-574-15

Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wry 3
||| |
Db 3 WRY 5

RESULT 4

US-08-482-528-124
; Sequence 124, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-528-124

Query Match 57.5%; Score 23; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYR 4
Db 2 WRNR 5

RESULT 5

US-08-014-979-81
; Sequence 81, Application US/08014979
; Patent No. 5510240

; GENERAL INFORMATION:

; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014, 979
; FILING DATE: 19930208
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 81:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-014-979-81

Query Match 52.5%; Score 21; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYR 5
Db 2 WREKE 6

RESULT 6

US-08-240-511-1
; Sequence 1, Application US/08240511
; Patent No. 5643722

; GENERAL INFORMATION:

; APPLICANT: ROTHCHILD, Kenneth J.
; APPLICANT: SONAR, Sanjay M.
; TITLE OF INVENTION: METHODS FOR THE DETECTION AND ISOLATION OF PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,511
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 16865-0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-240-511-1

Query Match

50.0%; Score 20; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYR 3

Db 1 WKY 3

RESULT 7

US-08-907-403A-7
; Sequence 7, Application US/08907403A
; Patent No. 6013633

; GENERAL INFORMATION:

; APPLICANT: Balasubramaniam, Ambikaipakan
; APPLICANT: Chance, William T.
; TITLE OF INVENTION: Compounds For Control
; TITLE OF INVENTION: Of Appetite, Blood Pressure, Cardiovascular
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wood, Herron & Evans, L.L.P.
; STREET: 441 Vine Street
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45202-2917

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,403A
; FILING DATE: 07-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/023,588

; FILING DATE: 09-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Albainy-Jenei, Stephen R.
; REGISTRATION NUMBER: 41,487
; REFERENCE/DOCKET NUMBER: UOC-113A-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 241-2324
; TELEFAX: (513) 421-7269
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FEATURE:
; LOCATION: 3
; OTHER INFORMATION: Xaa represents Nva
US-08-907-403A-7

Query Match 50.0%; Score 20; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryr 4
Db 1 WRXR 4

RESULT 8
US-08-487-006-17
; Sequence 17, Application US/08487006
; Patent No. 5641861
; GENERAL INFORMATION:
; APPLICANT: Dooley, Colette T.
; TITLE OF INVENTION: Houghten, Richard A.
; TITLE OF INVENTION: No. 5641861el Mu Opioid Receptor Ligands:
; TITLE OF INVENTION: Agonists and Antagonists
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,006
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-Tp 1706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE: Peptide
; NAME/KEY: Peptide
; LOCATION: 1

; OTHER INFORMATION: /note= "Amino acid is acetylated at
; OTHER INFORMATION: the N-terminal."
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 6
; OTHER INFORMATION: /note= "Amino acid is amidated at
; OTHER INFORMATION: the C-terminal."
US-08-487-006-17

Query Match 50.0%; Score 20; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 wryr 4
Db 3 WMYR 6

RESULT 9
US-08-537-069-12
; Sequence 12, Application US/08537069
; Patent No. 5688912
; GENERAL INFORMATION:
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Peptide Ligands Which Bind to
; TITLE OF INVENTION: von Willebrand Factor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,069
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gibling, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-537-069-12

Query Match 50.0%; Score 20; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ryrey 6

Db 1 RYRSF 5

RESULT 10
US-08-488-659A-17
; Sequence 17, Application US/08488659A
; Patent No. 5919897
; GENERAL INFORMATION:
; APPLICANT: Dooley, Colette T.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: Mu Opioid Receptor Ligands:
; TITLE OF INVENTION: Agonists and Antagonists
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,659A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-TP 1705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "Amino acid is acetylated at
; OTHER INFORMATION: the N-terminal."
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 6
; OTHER INFORMATION: /note= "Amino acid is amidated at
; OTHER INFORMATION: the C-terminal."
US-08-488-659A-17

Query Match 50.0%; Score 20; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYR 4
; I I I
Db 3 WYR 6

RESULT 11
US-08-305-768-27
; Sequence 27, Application US/08305768
; Patent No. 5602097
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,768
; FILING DATE: 12-SEPT-1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-305-768-27

Query Match 47.5%; Score 19; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYR 3
; I I I
Db 1 WRF 3

RESULT 12
US-08-871-163-27
; Sequence 27, Application US/08871163
; Patent No. 5885782
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,163
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-871-163-27

Query Match 47.5%; Score 19; DB 2; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYR 3
; I I I
Db 1 WRF 3

RESULT 13
US-08-767-903-27
; Sequence 27, Application US/08767903
; Patent No. 6020312
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,903
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-767-903-27

Query Match 47.5%; Score 19; DB 3; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0;

Qy 1 WRY 3
||:
Db 1 WRF 3

RESULT 14
PCT-US95-11724-27
; Sequence 27, Application PC/TUS9511724
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11724
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-11724-27

Query Match 47.5%; Score 19; DB 4; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0;

Qy 1 WRY 3
||:
Db 1 WRF 3

RESULT 15
US-08-165-545-7
; Sequence 7, Application US/08165545
; Patent No. 5424396
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial peptide and
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,545
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,981
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-7

Query Match

47.5%; Score 19; DB 1; Length 4;

Wed Nov 8 07:33:31 2000

09-258947-1.closed.rai

page 7

Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wryr 4
I:1
Db 1 WQWR 4

Search completed: November 8, 2000, 07:27:43
Job time: 100 sec

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